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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

JOURNAL MEDLINE COMMENT	TITLE	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 STACNA LOCUS DEFINITION ACCESSION
Staphylococcus aureus collagen adhesin [published erratum appears in J Biol Chem 1994 Apr 15;269(15):11672] J. Biol. Chem. 267 (7), 4766-4772 (1992) 92165839 On Aug 30, 1993 this sequence version replaced gi:386712.	Patt1.7.M., Jonsson,H., Guss,B., Switalski,L.M., Wiberg,K., Lindberg,M. and Hook,M. Molecular characterization and expression of a gene encoding a	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. 1 (bases 1 to 3827)	M81736.1 GI:387879  M81736.1 GI:387879  Staphylococcus aureus DNA.  Staphylococcus aureus	STACNA 3827 bp DNA BCT 17-AUG-1994 Staphylococcus aureus collagen adhesin (cna) gene, complete cds. M81736

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TVHKSEAGTSSVFYYKTGDMLFEDTTHYWMTLNINNEKSYVSKDITIKDQIQGQQLD
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VLKQDKDTKAPIANVEKLSKKDGSVVKDNQKEJEIITDANAGIANIKALPSGDYILKE
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NKYTPKRONKELY PEKERDKTPPTKPDHSNKVKETPPDKPSKVDKDDQPKDNKTKPEN
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GQQVKYTVEELTKVKGYTTHVDNNDMGHLIVTNKYT PETTSISGEKVWDDKDNQDGKR
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IYKLYKQDDNQNTTPVDKAEIKKLEDGTTKVTWSNILENDKNKEKIKYLVKEVVAAQG
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KVKTLDVTSETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDINGTIITNKYTFGE
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Hybrid
coding
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                                                                                                                                                                                                                           activity.
A18434
A18434.1 GI:513301
                                                                                                                           Patent:
                                                                                                                                                               artificial sequence.
1 (bases 1 to 3468)
                                                                                                           COLLAGEN BINDING PROTEIN AS WELL atent: WO 9207002-A 1 30-APR-1992; Location/Qualifiers
                                                                                                                                                                                                                                                              DNA molecule comprising a nucleotide sequence from S for a protein or polypeptide having collagen binding
                                                                                                                                                                                                                                                                                                                                                                                849
                                        translation"
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1. 346%
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                                                   /note="Protein sequence
                                                                                                                                                                                                                                                                                         3468 bp
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                                                   conflict with
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OLVKTYNDELTKNGYTHVDNDMGNLTVTNNYFTNGTHTWFTGLDEKAKG
OLVKTYNDELTKNGYTHVTNTNTTNTNTTWFTGLDEKAKG
OLVKTYNDELTKNG

SAGOROGH OLVKTNTNTNTNTNTN
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õ 밁 õ 밁 Qy В Ş 밁 Ş 뫄 Š 밁 γQ 밁 δÃ 밁 Qy 밁 δÃ 망 20 Matches Query Match Best Local 595 475 514 454 334 415 394 301 181 214 154 241 274 121 Local Similarity 61 94 GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180 AACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAATTTTTCAATTAAC GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAGTGGCATGGCCGACAAGC GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT AGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGAT AGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAAGGTGGACAGCAGTTAGAT A--CGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTTCTATTATAAAA----CGGGAG ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGCAA GGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG 836; Conservative 93.3%; 0, Score 792.2; DB 6; Pred. No. 5.3e-127; Mismatches Indels Length 6; Gaps 654 594 534 153 693 633 453 573 474 333 120 355 393 300 213 60 <u>س</u>

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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ORIGIN
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Best Local Similarity
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assembled sequence from
A18436
A18436.1 GI:513303
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Location/Qualifiers
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                                          Conservative
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931. .4488
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a 676 c 868 g 1122 t
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/transi_table=11
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/protein_ide="canol396.1"
/db_xref="GI:513304"
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                                                            93.3%;
                                        0;
                                        Score 792.2; DB 6;
Pred. No. 5.1e-127;
0; Mismatches 13;
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                                          Indels
                                                                                Length 4612;
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                                        6,
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RESULT 5 AR067712 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Qy Db 1	Qу Db 1	Qy Db 1	Ωy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Оу Въ 1	Qy Db 1	Qy Db 1	Qу Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Db 1
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AR067712 4612 bp DNA PAT 29-SEP-199 Sequence 8 from patent US 5851794. AR067712 AR067712.1 GI:5998934 . Unknown. Unknown. Unclassified. 1 (bases 1 to 4612) Guss, B., Hook, M., Jonsson, H., Lindberg, M., Patti, J., Signas, Switalski, L.	GATAAAGATACCAAG 849 	ATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAG 8 	TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATAC∱GTGCACAAT 7 	TACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGG 7 	AACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC 6	GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG 5 	TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT 5 	AGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGAT 4 	ATATGCTACC-AGAAGATACGACACATGTACGATGGTTTTAAATATTAACAATGAAAAA 4 	ACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAG 3 	ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 3 	AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGCAA 2 	GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 1 	GGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG 1 	
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                                                      ATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTTAAAACAG
                                                                                                               TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAAT
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                                                        GAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAG
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Trypanosoma brucei chromosome II o
IN PROGRESS ***, 1 ordered pieces
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On Jul 17, 2001 this sequence version replaced gi:12746529
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
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AC007926.8 GI:14787210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is believed to be correct as given, however the of the gaps between them are based on estimates provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is availably the finished sequence as soon as it is available preserved.

1 155204: contig of 155204 bp in length
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                       AATATTAACAATGAAAAAAGTTATGTATGGAAAGATATTACTATAAAGGATCAGATTCAA 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-OCT-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
On Dec 11, 2000 this sequence version replaced gi:11230847.

* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
are represented as runs of N. The order of the sizes
tis believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

This sequence will be replaced
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1 (bases 1 to 171798)

1 (bases 1 to 171798)

El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K. El-Sayed, N.M., Ghedin, E., Song, J., Miltscher, J., Pai, G., Van Peterson, J., Hou, L., Zhao, H., Mason, T., Miltscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Aken, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Milte, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTatill. 1 RPC193-1118 BAC genomic sequence
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Trypanosoma
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Trypanosoma brucei
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1 171798: contig of 171798 bp in length.
Location/Qualifiers
1. 171798
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                                                                                        Conservative
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                                                                                                                                                                                                                        /chromosome="unknown"
/clone="RPCI93-1118"
37575 c 33263 g 6
                                                                                                                                                                                                                                                                                                                   /organism="Trypanosoma
/isolate="GUTat10.1"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:5691"
                                                                                                           7.7%;
                                                                                   Score 65.6; DB 2;
Pred. No. 0.016;
0; Mismatches 234,
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                                                     GGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCT 340
                                                                                                        AAGGAAGAATTTAACGCAAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTG
                                                                                                                                                            TTAAAAGTTTTAAAACAGGA 836
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166494
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
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577 ACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATAT 636
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                                                                                                             GGTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAAT 516
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                                                                      TATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATA
                                                                                                                                                                                                                                                              209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-JUN-1999) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA On Jul 17, 2001 this sequence version replaced gi:12746529.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the sizes for the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., V Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E. Melville, S., White, O., Adams, M.D., Donelson, J. E. and Fraser, C.M. Trypanosoma brucei GUTatl0.1 RPCI93-3H15 BAC genomic sequence
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Trypanosoma brucei
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1 (bases 1 to 155204)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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by the finished sequence as soon as it is available
the accession number will be preserved.
1 155204: contig of 155204 bp in length.
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/chromosome="II"
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5, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0345C21.

* NOTE: This record contains 253 individual

* NOTE: This record contains 253 individual

* contigs. Runs of Nare used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 208546) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-OCT-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 AAATAACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGGT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ACAATTACATTCAATGATAAAGTAGAAAAATTAAGTGATGTTTCGGGATTTGCAGAATTT 213
                                                                                                                                                                                                                                                                                                                                                    812 GTGAATTAAAAGTTTTAAAACAGGATAAAGATACCAAG 849
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                                                                                                                                                                                                                                                                                                                                                                                   CATTTAATCATACTGTGCACAATATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAG 811
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Naliapareddy, S.R., Singh, K.V., Duh, R.W., Weinstock, G.M. and Murray, B.E.
Diversity of ace, a gene encoding a microbial surface component
                                                                                                                                                                                                          AF260878 1822 bp DNA BCT 1
Enterococcus faecalis strain LBJ-1/TX0020 collagen
                                                                                      Enterococcus faecalis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                precursor (ace) gene, complete cds AF260878
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                                                                                                                                                                                                                                                                                                                                                                  234 GACAAAGAGAATCAGAAAATAAAAACCTGGAGATACTATTACTTTAACTTTGCCAGGTGCA 293
                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                            1 GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAGTGGCATGGCCGACAAGC
CCGAATGTGATAGAAACGGATTTCGGAACAGCAACGGCGACTCAACGTTTGACGATTGAA
                                          ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 300
                                                                                                                AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAAGTTAACGCAA 240
                                                                                                                                                                                                                            GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180
                                                                                                                                                                                                                                                                         TTAGTTGGAATGACCGAGAACGATGGTTCACCACGAAAAATCAATTTAAATGGTTTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         247;
                                                                                         CATAATGTGAATGGGCATTTTTCTTTCGGGATTAAAACGCTTATCACCAATAGTTCGCAA
                                                                                                                                                                                  GAAGTTTTTATCTATAAAGATCATGTTGTAGCAACATTTAACGAAAAAGTTGAATCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recognizing adhesive matrix molecules, from different strains of enterococcus faecalis and evidence for production of ace during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murray, B.E.
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1107. 1787
/gene="ace"
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TEESLDIPLETILEEWEPKTPTSEQATETSEKTDYTETVDSSQPEWHVSPTEEBHDES
ETLGTISPIIPEENGATETAESSQPEVHVSPTEDEWHVSPTEEBHLDESETLGTISPIP
EKPSVTTEENGATETAESSQPEVHVSPTKEITTEKKQPSTETTVETNKTITSKNQPQ
ILNAPLNTLKNEGSPQLAPQLLSEPIQKLNEANGQRELPKTGTTKTPFMLIAGILAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="collagen adhesin precursor"
/protein_id="AAG23936.1"
/protein_id="AAG23936.1"
/db_xref="Gi:10863216"
/translation="MTKSVKFLVLLLVMILPIAGALLIGPISFGAELSKSPIVDKVEL
/translation="MTKSVKFLVLLLVMILPIAGALLIGPISFGAELSKSPIVDKVEL
DHTTLYOGEMTSIKVSFSDKENOKIRPGDTITLTLEGALVGMTENDGSPRKINLNGLG
EVFITYOHVVATFNEKVESVHNVNGHESFGIKTLITNSSQPNVIETDFGTATATORGEG
EVFITYCHTVATFNEKVESVHNVNGHESFGIKTLITNSSQPNVIETDFGTATATORGEG
OQLNKESFTFDIVNDKETKYISLAEFEDQGYGKIDFYDNDFNLRFYRDKARFTSFIV
OQLNKESFTFDIVNDKETKYISLAEFEDQGYGKIDFYDNDFNLRFYRDKARFTSFIV
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141. .1109
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518 ATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAAGCCTTTCCAGGTTCTAAAATAA 577
                                                                                                                                                                         398 ATATTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714 AAAGAGAGTTTTACATTTGATATTGTGAATGACAAAGAAACTAAATATATTTCAC 768
                                                                                    GTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATT 517
                                                                                                                                  TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGAC 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATATGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTA-----TTATAAAACGGGA 354
                                         GGCGATTTGGCTGGAGAGTCAAATCAAGTACGTTGGTTTTTAAATGTGAACCTCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on Aug 24, 1999 this sequence version replaced g1:5731882. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: The sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB10 1SA, t
On Aug 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage etc.

Order of segments is not known; 800 n's separate segments

NOTE: This is a 'working draft' sequence.

NOTE: This is a 'working draft' sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 318221)
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Plasmodium falciparum chromosome 13 strain
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/chromosome="13"
29264 c 27321 g 11:
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/strain="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                       Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission Submitted (21-AuG-1998) Stanford DNA Sequencing and Techn Center, Stanford University, 855 California Avenue, Palo
                                                                                                                                                                                                                                                                                                                                                                          94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum 3D7 chromosome 12
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Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B.
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AC005504.3 GI:4558584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                       n Apr 2, 1999 this sequence version replaced gi:4337172. NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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91212
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                   /organism="Plasmodium
/db_xref="taxon:5833"
/chromosome="12"
                                                                                          ocation/Qualifiers
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                                                                             .104992
 9326 c
                                                                                                      58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length
9564 g
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Gaps

7.2%; 43.6%;

Score 61.4; DB Pred. No. 0.088;

Length 104992; Indels

Best Local Similarity

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                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; 1 (bases 1 to 169546)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W. Direct Submission Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology
                                                                                                                                                                                      HTG; HTGS_PHASE1.
malaria parasite P. falciparum
                                                                                                                                                                                                                                                        Plasmodium falciparum chromosome 12 clone PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                        Plasmodium falciparum
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                                 GATGTA---ACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACAAA 660
                                                                                                                                                                                                                                                                              TCGAAAGATATTACTATAAAGGATCAGATTCAAGGTTGACAGCAGTTAAGATTTAAGCACA 483
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                                                                                                                                                                    AAAAATAACATTGAAAAAATGATAATAATCATAATAGCAAAAATAATGAATATAATGAG
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AATGTATAATAGTGATAAAATATCTTTTCAAAATCAACCTGAAATAATTTACTCAAAT
                                                                                                                          GATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACACAATT 603
                                                                                                                                                                                                          TTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATTACT
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                                                                                                                                                                                                                                                                                                                                          TCAGATGATGTCAAAATATTTAATGAGAATTCAAATAATGAAAATAAGAAAAAGGTGAAA 7535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGAATCAAAAATAATGGATGAAGAAAATATCCAATTAGAAAAACAAAAATATATCTTTA 7523
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                                                                               AATACGAAAAAAGATGAACAAAGTACGGTACTATTCTTAGATGACGTCAAAAAAAGAACAA 75535
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* consists of 2 contigs are true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center, St. 94304, USA
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69871 a 15381 c 1
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Fragment Name Beyin End PFMAL4P1 1 11000

PFMAL4P1 1 10001 210000

PFMAL4P1 2 100001 210000

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Continuation (2 of 4) of PFMAL4P1 from base 100001 (AL034557 Plasmodium falciparum chrom
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Best Local Similarity 44.0%;
31725 AGGAAGATTTTATTGATTTTAAAGAAAATAT 31755
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                                      764 CTGTGCACAATATTAATGCTAATGCCGGTAT 794
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE ACCESSION VERSION KEYWORDS RESULT CNS06X9S REFERENCE SOURCE DEFINITION JOURNAL MEDLINE TITLE ORGANISM TITLE JOURNAL AUTHORS AUTHORS 2 (bases 1 to 1007)
2 (bases 1 to 1007)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozler-Kalogeropoulos,O., Potler,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000) CNSU6X9S 1007 bp DNA GSS 06-JUL-2001 T3 end of clone AXOAA039F08 of library AXOAA from strain CBS 7064 of Pichia farinosa, genomic survey sequence. Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux; CP 5706, 91057 EVRY cedex, FRANCE. (E-mail 1 (bases 1 to 1007)
de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Potier, S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia FEBS Lett. 487 (1), 87-90 (2000) 20584725 Pichia farinosa AL419462.1 GSS. Genoscope sorbitophila Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia. Pichia farinosa. (bases 1 to 1007) GI:12202640 (E-mail :

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CNS00EVL 1101 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (from Drosophila melanogaster)
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This GSS is part of a random genomic sequencing program of thirteen
Yeast species: Saccharomyces bayanis var. uvarum, Saccharomyces
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/db_xref="taxon:4920"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  El-Sayed, N., Zhao, S., Zha
Gerrard, C., Leech, V., de
, Fraser, C. and Adams, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
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Other_GSSs: Sheared DNA-46J23.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Sheared DNA-46J23"
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL108811
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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fruit fly.

fruit fly.

Fruit fly.

Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Plasmid Drosophila; Mengeda; Arthropoda; Tracheata; Hexapoda; Inse

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                  ATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACAAAAACCA 664
                                                                                                                                              TAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATTACTG
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ATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACACAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                         - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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                             AACATCTGGGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAG
                                                                                                TGAAGTACAAGGAAGAATTTAACGCAAACAAATACTTCAGATGACAAAGTAGCTACGAT 272
AARATAGWGAWADKKAKWAAAAAGKTRAAKRGWAAAAAAAAAAAAAAATAAAAAAAAAAGKAA 664
                                                               AAAAGAAAAAAAAAGTWAATAAAAAAAAAAAATATGTGAAAKAWAAAAATATAGTAWAA 724
                                                                                                                                 ATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAGGATAAAGATA 844
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                                                                                                                                                                                                    271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Anopheles gambiae GSS T7 end of clone 14D07 of NotreDamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP 191 91006 EVRY cedex - FRA
- Web : www.genoscope.cns.fr)
2 (bases 1 to 879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-FEB-2000) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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licoidea; Anopheles.
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/note="end : T7"
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/clone="14D07"
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/strain="PEST"
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila n
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/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone="BACN13C23"
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TTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAAC 578
                                                                                                                TGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTA 518
                                                                                                                                                      TATTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/clone="BACN10102"
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High quality sequence stop: 2
Location/Qualifiers
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T24D11-Sp6 TAMU Arabidopsis thallana genomic clone
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Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ecker J.
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                                                                                                                                               /note="Vector: BeloBACII; Site_1: HindIII; 
; Produced by Rod Wing" 
50 c 53 g 678 t 372 others
                                                                                                                                                                                                                                                          /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                              /sex="hermaphrodite"
                                                                                                                                                                                                                /clone_lib="TAMU"
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/clone="T24D11"
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                                                                           7.1%;
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Fruit fly.

Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Plasmid Drosophila; Insecta;

Plasmid Drosophila; Plasmid Metazoa; Arthropoda; Tracheata; Hexapoda; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1204)
              - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 BACN15A12 of DrosBAC library from Drosophila melar
                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequenca; BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns
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BP 191 91000 BYNE CONS. FT)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
                                                                                              Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                       150 AAATARTTWAAAGACAARAAGAACAAAAAAAAAAAAAAAATAAGWAAATAAAWATATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 AACAATGAAAAAAGTTATGTATCGAAAGATATTTACTATAAAGGATCAGATTCAAGGTGGA 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569 AAAAAAAWAAWWAATAAAAAAAAAAAAAAAAAATAAARAATAAAAAAWAAATTATAAAAT 510
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   30
   AATTAAAAATTGAAAAAA
                                                                GTTTTAAAACAGGATAAA 840
                                                                                                                                                                                                           ACTGTGCACAATATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAA
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                                                                                                                                           AAAGAACACCCCATAAGAGTGTAAGGCGTGARTAWTTGATTAAAAAGAAAAAAAATAATA
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                                                            AATAGTTTTCAATTAACTACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGGACAGCAGTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAAT 516
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Determination of clone end sequences from Trypanosoma brucei GUTat
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Other_GSSs: Sheared DNA-42E21.TR
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/strain="REEU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-42E21"
/clone="Sheared DNA-42E21"
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                        184 TTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAATTTAACGCAAACA
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                                                                                                                                                                                                                  ACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAAACTGTTAAAGGTGAACAGGTG 123
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                                                                         GGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAAAAA 183
                                                                                                                                                                      rraaaarrardarararararrarakaarargarrrgkrrrkgragrrrargaggr 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the BaC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS005TE 997 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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                                                                                                                                                                     NNTTTANTNTNNNNTTTNANATTNGACCTTNTCTATTTATTATTATTATTAWACMTTNN 299
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Search completed: January 29, 2002, 22:42:29 Job time: 4603 sec

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Result
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Perfect score:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
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DB
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S39004
E86706
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A48620
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cell surface antig
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rhoptry protein

RESULT 2 A48620 adhesin - Staphylococcus aureus (fragment) C; Species: Staphylococcus aureus C; Species: Staphylococcus aureus C; Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mag-1995 C; Accession: A48620 R; Patti, J.M.; Boles, J.O.; Hook, M. Biochemistry 32, 11428-11435, 1993 A; Title: Identification and biochemical characterization of the ligand binding A; Reference number: A48620; MUID:94032261 A; Contents: FDA 574 A; Accession: A48620	Qy 12 SDDKVATITSGNKSTNVTYHKSEAGTSSYFYY-KTODM-LPEDTTHYRWFLAINNEKSYV 69	ap db	30 90.5 8.1 784 2 JH0101 appolipoprotein B-1 31 90 8.0 669 2 S14535 asparagine-rich pr 32 90 8.0 858 1 A42239 33 90 8.0 4688 2 F82885 34 89.5 8.0 416 1 A41267 35 89.5 8.0 496 2 T26296 36 89.5 8.0 1496 2 T26296 37 89.5 8.0 1815 2 C81169 40 89 7.9 570 2 T46261 41 89 7.9 570 2 T46261 42 89 7.9 1166 2 T28640 43 89 7.9 1166 2 T286940 44 89 7.9 1146 2 T2852 45 ALIGNMENTS  ALIGNMENTS

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submitted to the EMBL Data Library, December 1993
A; Reference number: S42798
A; Accession: S42798
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1092 <SIG>
A; Cross-references: EMBL: Z29088; NID: 9436135; PIDN: CAA82330.1;
C; Keywords: fibronectin binding
                                   A; Experimental
                                                                                                                                    A; Reference number: A86625
A; Accession: D86710
                                                                                                                                                                              Genome Res. in press, 2001
A; Title: The complete genome
                                                                                                                                                                                                                                                        collagen adhesin {imported} - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
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A;Note: sequence extracted from NCBI backbone (NCBIP:138726)
A;Gene: icaC
                                                      A;Cross-references: GB:AE005176; NID:g12723592; PIDN:AAK04782.1; GSPDB:GN00146
                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                  R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach,
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                                   source: strain IL1403
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Pred. No.
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RESULT 5
A43855
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Date: 10-Mar-1995 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Date: 10-Mar-1995 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Date: 10-Mar-1995 
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Nature 404, 502-506, 2000
                                                                                                 probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis
C;Spectes: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81888
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1536 <BAR>
A;Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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                                                                                                                                                                                                                                                                                                                                                                                                                                  KEEVNGKSFNHTVHNINANAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSKNLSITTNSSSTYRTI-----ISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      193
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Pred. No. 26;
33; Mismatches
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Pred. No. 0.16;
28; Mismatches
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                                 S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1536;
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                                 S.R.; Mo
Rajandre
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A; Title: Complete DNA sequence of a A; Reference number: A81775; MUID:203

MUID:20222556

serogroup A strain of Neisseria

menigitidis

Z2491

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A:Status: r--
A:Mocule type: DNA
A:Residues: 1-4919 <WAR>
A:Residues: EMBL:AF057696;
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C:Species: Haemophilus ducreyi
C:Date: 22-Oct-1999 *sequence_revision 22-Oct-1999 *text_change 22-Oct-1999
C:Accession: T31105
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like prote
A;Reference number: Z20984; MUID:99030326
A;Accession: T31105
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-592 < PAR>
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Best Local S
Matches 43
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                                                                                    1200
                                                                                                                                                                1147 FENNMQ-SQKVDLYTKIFEAKSDIELTFKTNGTHPVYLNFKS--NNNEKKYRNS----EN 1199
                                                                                                                                                                                                                                                1104 RIGKIYAGR---DLTFNKSNAGGKS-----EIINRGT----INVKNKLSYDS-DVS 1146
                                         174
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                                                                                                                                                                                                                                                                                     15 KVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT 74
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                                       EVNGKSFNHTVHNINANAGIEGTVKGE-LKVLKQ 206
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-- NPHYLNTALKHILGNGWQDDLKKQENIKVLKQ 1282
                                                                                TKNFKSIGDLINEALSDSAPEAIEAYYSGSSSNYINPVSYLAALGNANNSS:
                                                                                                                     TKN-----TIDVTIPQGYGSYNS-FSINYKTKITNEQQKEFVNNSQAWYQEHGKE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNHTVHNINANAGIEGTVK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGK-----GKGE-NGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGST-----LTDTLAGSSASHV--- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DAGNQSTHYTRAASIKDVLNAGW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                 h 8.8%; Score 98.5; DB 2; Similarity 24.8%; Pred. No. 1.4e+02; 53; Conservative 34; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99.5; DB Pred. No. 8.5; 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g3929021; PID:g3929023; PIDN:AAC79761.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIKGVKTGSTTGQSENVDFVRTYDTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                        Length 4919;
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                 12;
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RESULT S33851

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69

VSK-DITIKDQIQGGQQLDL----STLNINVTGTH---

-SNYYS 103

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA topoisomerase I (topA) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Start codon: TTG
C;Keywords: fibronectin binding
E;1-27/Domain: signal sequence #status predicted <SIG>
F;28-1117/Product: fibronectin-binding protein #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1117 <LIN>
A;Residues: 1-1117 <LIN>
A;Cross-references: EMBL:Z22151; NID:g288970; PIDN:CAA80122.1; PID:g581643
A;Note: the authors translated the initiation codon TTG for residue 1 as La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lindgren, P.E.; McGavin, M.J.; Signaes, C.; Guss, B.; Gurv
Eur. J. Biochem. 214, 819-827, 1993
A;Title: Two different genes coding for fibronectin-binding
A;Reference number: S33850; MUID:93307299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibronectin-binding protein precursor - Streptococcus dysgalactiae C;Species: Streptococcus dysgalactiae C;Species: Streptococcus dysgalactiae C;Date: 31-Dec.1993 #sequence_revision 02-Aug-1994 #text_change 15-Oct-1999 C;Accession: S33851; S32631
                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001180; GB:AE000783; NID:g2688755; A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type; DNA_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY
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                                                                                                                                                                                                                             C;Superfamily:
                                                                                                                                                                                                                                                                                                       A; Residues: 1-848 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: C70203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: fnbB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S33851
                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 NTIDVTIPQGYGSYN-----SFSINYKTKIT----NEQQKEFVNNSQAWYQEH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 NINYNAGGSRTDSV-YAKSGVLDDFDSTGRIVNWYFNFNAALNPI-KDEDVEFMTTDNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 IEWNLDKNQFGAKVRIQRSGSWILGVRPGDLKVLKFERD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 GKEEVNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 QTMTWDIEAVKKDPYVVQIRGGYLGTVFSKNGGWIDIEEATKLGIEIIFSGQKLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 NVTVHKSEAGTSSVFYYKTGDMLPEDTTH--VRWFLNINNEKSYVSKDITIK----DQIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GGQQLDLSTLN----INVTGTH-SNYYSGQSAITDFEKA-----FPGSKITVDNTK 126
IKKGDTFSIVKMKTSEHETKAPFRYTEASLVQKMEKEGIGRPSTYSTI---ISTLLEREY 513
                                                  ITSGNKSTNVTVHKSEAGTSSVFYY------KTGDMLPEDTTHVRWFLNINNEKSY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IKIPK-WTNYNGLIPYVKPLNQTSISVKLTAKITEKTMRDQTIEYVENDSIPKIEG
                                                                                                                           Similarity
                                                                                                                                                                                                                             bacterial type I DNA topoisomerase
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                         8.6%;
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23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Mismatches
                                                                                                 41; Mismatches
                                                                                                                         Score 96.5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 98; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                spirochaete,
                                                                                                                                                   DB 2;
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                                                                                                    84;
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                                                                                                                                                   Length 848;
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                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                         translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi.
                                                                                                                                                                                                                                                                               PIDN:AAC67161.1; PID:g268
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                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                 Gaps
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                                                                                                    14;
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finger protein MSN2 - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein YM9532.02c; protein YMR037c
C;Species: Saccharomyces cerevisiae
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 21-Jul-2000
C;Accession: S39004; S52886; A48131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 269, 11987-11992, 1994
A;Title: Conserved domain structure of beta-neurexins. Unusual cleaved signal sequences A;Reference number: A53580; MUID:94216308
A;Accession: A53580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
A53580
                                                                                               A; Reference number: A48131; A; Accession: S39004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurexin III beta precursor (clone pB794-7) - bovine C;Species: Bos pringenius taurus (cattle) C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 17-Mar-1999 C;Accession: A53580
submitted to the EMBL Data Library, February 1995
A; Reference number: S52885
                                 R;Odell,
                                            A;Cross-references: EMBL:L08838; NID:g349594; PIDN:AAA34806.1;
                                                              A; Molecule type: DNA
A; Residues: 1-704 <EST>
                                                                                                                             A; Title: Two homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
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A;Molecule type: mmNA
A;Residues: 1-392 <USH>
A;Cross-references: GB:L27864
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                                                                                                                                            Estruch, F.; Carlson,
ol. Cell. Biol. 13, 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                           199 NTDNERFQMVKQKIPFKYNRPVEEWLQEKGRQ-----LTIFNTQAQIAIGGKDKGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
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                                c.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WFLN----INNEKSYVSKDITIKDQI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                        NVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSIN--YKTK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEHHFHGSK------HHSVPISIYRSPVSLRGGHAGATYIFGKSGGLIL-----YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEYTKKGKPKKLKIIKAKK 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKKGLKDTVMQLEPKIDSSEFRTVIESQKI----ENKNSINYTINIGKYGPYLIFKGHNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHHHHHGSDDKVATITSGNKSTNVTVHKS-----EAGTSSVFYYKTGDMLPEDTTHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INAKTPLENLYKKDETEKTINEKELKPNILGVDPLTGLNVIFKNTIYGNIVQLGEDTHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INYKTKITNEQQKE----FVNNSQAWYQEHGKEEVNGKS--FNHTVH-NI-----NANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQSAITD------FEKAFPGSKITVDNTKNTIDVTIPQG-YGSY----NSFS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                Bowman, S.
                                                                                                          13, 3872-3881, 1993
cologous zinc finger genes
per: A48131; MUID:93309420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No.
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A;Cross-references: GB:AE005176; NID:g12723558; PIDN:AAK04751.1; A;Experimental source: strain IL1403 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
E86706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625 A;Accession: E86706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ygeA [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Keywords: DNA binding; nucleus; transc. F:649-665/Region: zinc finger CCHH motif F:678-698/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S52886
A;Molecule type: DNA
A;Residues: 1-704 <ODE>
A;Cross-references: EMBL:Z48502; NID:g695715; PIDN:CAA88403.1; PID:g695717; GSPDB:GN0
C;Genetics:
C;Genetics:
A;Gross-references: SGD:S0004640; MIPS:YMR037c
A;Cross-references: SGD:S0004640; MIPS:YMR037c
                                                                                                                                                                                                                                                                                                                                             A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 13R
C; Superfamily: finger protein MSN2
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-359 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. in press, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Bolotin, A.; Wincker, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: E86706
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 RRFSDV-ITNQFPSMTNSRNSISHSLDLWNHPKINPSNRNTNLNIT-TNSTSSSNASPNT 342
                                                                                                         76
                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                         19 ITSGNKS---TNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                             KTDAEGIKKGDIVTIKVKRKPTNILGVYIMSGNVQSKKSNIKQHSKS--NNEPSNSNTKK
                                                                                                     KDQIQGGQQLDLSTLNI-----NVTGTH----SNYYSGQSAITDFEKAFPGSKITVDNTK- 126
                                                                                                                                               LTYMNSSPDYTSVSVFKKDLDDDKNVVGKTFEFKVTDRTETS--INADDEISF----FTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DL-VNKQDEDPK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAMTKINPSQQLQQQLNRVQHKQLTSSHNNSSTNMKSFNSDLYSRRQRASLPIIDDSLSY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYKTKITNEQQ-KEFVNNSQ--AWYQEHGKEEVNGKSFNHTVHNINANAG---IEGTVKG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTMNANADSNI-AGNPKNNDATIDNELTQILNEYNMNFNDNLGTSTSGKNKSACPSSFDA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFEKAFPGSKITVDNTKN---TIDVTIPQGYGSYN------SFSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DITIKDQIQG------GQQLDL-----STLNINVTGTHSNYYSGQSAIT 109
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                                                                                                                                                                                                                                     58;
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21.7%;
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25.4%;
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                                                                                                                                                                                                                                                    Score 95; DB Pred. No. 9.6;
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Pred. No.
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-NTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV
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                                                                                                                                                                                                                                     84;
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A; Molecule type: DNA
A; Rosidues: 464-2020 <MOS>
A; Residues: 464-2020 <MOS>
A; Cross-references: GB:D85081; NID:g3041754
A; Cross-references: Strain K-12
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:88089, NCBIP:88090)
R; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.
A; Rose, D.J.; Man, B.; Shao, Y.
A.; Rose, D.J.; Man, B.; Shao, Y.
                                                                                                                                                                                                                                                             ABC-type transport protein ydbA.2 - Escherichia coli
C;Specles: Escherichia coli
C;Specles: Escherichia coli
C;Date: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 08-Oct-1999
C;Accession: C48399; D64891; H64891
R;Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
A;Reference number: A48399; MUID:92190338
A;Accession: C48399; MUID:92190338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chu, C.P.; Kariyama, R.; Daneo-Moore, L.; Shockman, G.D.
J. Bacteriol. 174, 1619-1625, 1992
A;Title: Cloning and sequence analysis of the muramidase-2 gene from Enterococcus hirae.
A;Reference number: A42296; MUID:92165737
A;Accession: A42296
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A; Residues: 1-666 < CHU>
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A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID: 97426617
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                                             Science 277, 1453-1462, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKLTIK----GGQSAGSSTTNTGNNASSGNTSGNTNTSGSTGQAT-----GAKYTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHNINANAGIEGTVKGELKVLKQDKDT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGNTSSNTANTGSTTSGSTYTVK 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSGDSVWKIANDHG-----ISMNQLIE-WNNIKNNFVYPGQQLVVSKGSSSASGSTSNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSGNSGGSATT-----TGTTYTVKSGDSV-WGISHSFGITMAQLIEW-NNIKNNFIYPG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSGDKFSKNYEGDFNNLLDSIKYTKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 95; DB
Pred. No. 21;
28; Mismatches
                                                                                                                                                                                                                                                                                                                     the replication terminus in Escherichia
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                                                                                           Riley,
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A;Molecule type: DNA
A;Residues: 1-2902 <ARN>
A;Cross-references: GB:AE001464; GB:AE001439; NID:g4154789; PIDN:AAD05855.1; PID:g415
A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric A; Reference number: A71800; MUID:99120557 A; Accession: C71953
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999 (;Accession: C71953 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; I'ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V. Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                           Вb
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A; Variety: strain J99
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A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 'M', 915-2020 <BLA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-839, 'LDLPLYFQTSVIT' <BLA1>
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A;Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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Best Local Similarity
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Best Local Similarity
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                                           1335 NLSQNASINASNHSTLEL----QGDLNLNDTSS----LNLNQSAINVSNNATINDYASLI 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 VNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 ATVDN-KGTMTVTDPESMGIQIDGDKAIVNNEGESTITNGGTGTQINGDDATANNNGKTT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 NGELVITGDNATVNNNGKTTVDGKDSTGTEINGNNGK-VIQDGDLDVSGGGHGIDITGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 TLTIRDSVFTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSADGATKWQYNH
  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GQQL----DLSTLNIN------VTGTHSNYYSGQSAITDFEK-----AFPGSK 119
                                                                                      23 NKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 GTS---SVFYY---KTGDMLPEDTTHVRWFLNI-----NNEKSY--VSKDITIKDQIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 HHHRNNSPLPPTPPDDESDDTPVPPTPGGDEIIPDDPDDTPTPPKPVSFNNDVILDKTEK 153
                                                                                                                                                                                                                                     jhp0274
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  IQGGQQLD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITVDNTKNTIDVTIPQGYG---SYNSFSINY--KTKITNEQQKEFVNNSQAWYQEHGKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                                                                                   Conservative
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25.1%;
                                                                                                                                                   8.4%;
23.1%;
                                                                                                                               26;
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  -LSTLNI----
                                                                                                                               Score 94.5; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95; DB
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jhp0274 - Helicobacter pylori (strain J99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVI-QDGD 354
  ----NVTGTHSNYYSGQSAITD- 110
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                                                                                                                                                                          Length 2902;
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                                                                                                                                   Indels
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                                                                                                                                   77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith,
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Db 1387 ASNGSHLNENGAVNENSANITTSLSSSSIVFKGAVSLRGOFNLSNNSSLDFQGSSAITSN 1446  Qy 111FEKAFPGSKITYDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV 160  Db 1447 TAFNFYDNAFSQSPITEHQALDIKVPLSLGGNLLNPNNSSVLNLK 1491  Qy 161 NNSQAWYQEHGKEEVNGKSFNHTVHNI 187  [   :	Sear Job	Db	Qy	DЬ	Qy	Db
ASNGSHLNENGAVNENSANITTSLSSSIVFKGAVSLRGOFNLSNNSSLDFQGSSAITSN 1446FEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV 160 ::	ch con time:	1492	161	1447	111	1387
	pleted: January 30, 2002, 00:03:33 2551 sec	-NSQLVFSDQGSLNIANIDLLSDLNGNKNRVYNI 1524	NNSQAWYQEHGKEEVNGKSFNHTVHNI 187		FEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV 160	:    :

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                     1122
1054.5
904
830
.178
165.5
125.5
116.5
116.5
                                                                                                                                                                                                                             Score
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length: 2000000000
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Match
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L: /SIDS8/gcgdata
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1122
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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 211
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AAW31557
AAW31557
AAW315567
AAW31667
AAB37668
AAW31556
AAW68150
AAW68150
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                                 Collagen binding p
Collagen binding p
Collagen binding p
Collagen binding p
Collagen binding A
Collagen binding A
Collagen binding A
Firbonectin-bindin
Clostridium botuli
Enterococcus faeca
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Enterococcus faeca
Enterococcus faeca
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666	667	329	1802	1802	1155	451	437	195	351	346	592	589	589	1536	1536	1536	1536	1095	537	1601	847	139	1529	342	1536	2314	493	1598	1338	184	1
				21	22	19	19	19	19	14	22	22	20	21	15	14	14	21		18	17	19	14	14	18	22	12	18	14	22	۲
AAR85291	AAB29654	AAW44778	AAY70119	AAY83170	AAG82343	AAW68398	AAW37738	AAW59053	AAW56000	AAR39493	AAU06180	AAU06173	AAY23745	AAB01846	AAR63505	AAR41725	AAR41723	AAB01847	AAP60452	AAW30292	AAW06400	AAW31556	AAR41732	AAR39498	AAW30293	AAB69136	AAR13992	AAW30291	AAR41731	AAB61673	MADICOCO
Enterococcus hirae	Human membrane-ass	Human recombinant	Staph. epidermidis	Cell wall protein	S. epidermidis ope	Clostridium bōtuli	Nucleotide sequenc		Fibroblast growth	Human apoAIV mutei	N. meningitidis 22	N. meningitidis P2	A surface protein	Haemophilus influe	Haemophilus high m	High molecular wei	High molecular wei	Haemophilus influe	Sequence of the As	Non-typeable Haemo	Class A starch bra	·Firbonectin-bindin	High molecular wei	Human apoAIV mutei	Non-typeable Haemo		P. falciparum spor	Non-typeable Haemo	High molecular wei	pQE60-Cys37 constr	United Not 7 Conser

## ALIGNMENTS

RESULT AAW31553

Collagen binding protein M31 epitope.

21-MAY-1998 (first entry)

AAW31553;

AAW31553 standard; Protein; 211

A

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Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRANM; adhesin; vaccine; immunisation; diagnosis; therapy; epitope M31.
      (UABR-) UAB RES FOUND.
(TEXA ) UNIV TEXAS A & M SYSTEM.
                               16-MAY-1996;
                                               14-MAY-1997;
                                                                20-NOV-1997
                                                                                 W09743314-A2
                                                                                                        Protein
                                                                                                                         Peptide
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                                                                                                                                                 Staphylcoccus
                                                                                                                                                  aureus.
                               96US-0017678.
                                               97WO-US08210
                                                                                                        /note= "vector pQE30-derived peptide"
13..211
                                                                                                                                Location/Qualifiers
                                                                                                /note= "epitope M31"
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AAW31554
ID AAW3
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XX COL!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This protein comprises Staphylococcus aureus collagen binding CDP protein (CBP) epitope M31, i.e. amino acids 61-343 of full-length CC BP, plus a vector-derived N-terminal peptide. Claimed 441, 849 cand 1500 bp nucleic acid sequences (see AAT93436-38) respectively commode CBP epitopes M17, M31 and M55 (see AAT93436-38) respectively commode CBP epitopes M17, M31 and M55 (see AAW31552-54) that confer commode CBP epitopes M17, M31 and M55 (see AAW31552-54) that confer composed commode CBP epitopes are contemplated in the creombinant production of the CBP composes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to compose the composition of pathological infections including acids as well as claimed anti-CBP antibodies will also be of use in composition and methods for the prevention of composition in an animal such as a human. The CBP content are also contemplated for use in the preparation of concines and as carrier proteins in vaccine formulations, as well carriers in fection.
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   Key
Peptide
                                                                                                                                                                     Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
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N-PSDB; AAT93437.
                                                                                          Staphylcoccus
                                                                                                                                                  epitope M55.
                                                                                                                                                                                                                                                                                                 Collagen binding protein M55 epitope
                                                                                                                                                                                                                                                                                                                                                             21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW31554 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31; Page 115-116; 143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVDNTKNTIDYTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHTVHNINANAGIEGTVKGELKVLKQDKDTK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tvdntkntidvtipggygsynsfsinyktkitneqqkefvnnsqawyqehgkeevngksf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 AA;
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                                                                                          aureus.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1122; DB 19;
Pred. No. 1.2e-86;
D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sthanam N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Symersky J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (CBP) epitope M55, i.e. amino acids 30-531 of full-length CC CBP, plus a vector-derived N-terminal peptide. Claimed 441, 849 cand 1500 bp nucleic acid sequences (see AAT93136-38) respectively cencode CBP epitopes M17, M31 and M55 (see AAW31552-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP cepitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in corrections, diagnostic and therapeutic applications including active and passive immunisation and methods for the prevention of contemplated for use in the preparation of contemplated for use in the preparation of sein the formulation of compositions for the prevention of s.
                                                                                                                                                                                                                                                                                                                Matches 211;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 31; Page 117-119; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-1996;
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protein (CBP) epitope M55
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                                                                                                                      121\ ltgtntsddkvatitsgnkstnvtvhkseagtssvfyyktgdmlpedtthvrwflninne
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              KNTIDYTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVH
                                                          ksyvskditikdqiqggqqldlstlninvtgthsnyysgqsaitdfekafpgskitvdnt
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kntidvtipggygsynsfsinyktkitneggkefvnnsgawygehgkeevngksfnhtvh
                                                                                          KSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNT
                                                                                                                                                                                    \verb|ptsgtvkiegysktvp|| tvkgeqvgqavitpdgatitfndkveklsdvsgfaefevqgrn||
                                                                                                                                                                                                                                                 mrgshhhhhhgsardisstnvtdltvspskiedggkttvkmtfddkngkiqngdmikvaw
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                                                                                                                                                                                                                                                                                                                                                                                           512 AA;
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13..512
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                                                                                                                                                                                                                                                                                                                             94.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus M55, i.e. amino acids 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "epitope M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "vector pQE30-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM
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                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                             Score 1054.5; DB
Pred. No. 1.8e-80;
0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                              DB 19;
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                                                                                                                                                                                                                                                                                                                                         Length 512;
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RESULT ADARS22675
ID ARR22675
ID ARR22675
XX AAR2
XX CBP;
YT Regiler R
                   The amino acid sequence (encoded by the sequence assembled from partially homologous pl6 and cCOLR6A inserts) comprises a structure resembling a signal sequence. Following this region, a region called A is found followed by a repetitive stretch of 187 amino acids called B1, B2 and B3. Directly following these regions there is a region called W which consists of a repetitive, hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                Guss BM, Hook M,
Switalski LM;
    structure contg. several proline residues.
                                                                                                                                                                                                                                                      Hybrid DNA molecule encoding S.aureus collagen binding protein protein is expressed in E.coli and used for diagnosis e.g. of
                                                                                                                                                                                                                                                                                                                                WPI; 1992-167099/20.
N-PSDB; AAQ24123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen binding protein
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                                                                                                                                                                                          Disclosure; Fig 2; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALFA ) ALFA LAVAL AGRI INT AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1991;
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/label= W
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1160..1179
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1180..1185
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30..1185
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This region is thought
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RESULT ANAI 1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to mediate the binding of the protein to the cell wall. The amino acid sequence nearest to the C-terminal end consists of a long stretch of hydrophobic residues followed by some charged amino acids This region is called M.

The CBP can be used for immunisation pref. in combination with a fusion protein, e.g. for vaccination of ruminants against mastitis caused by staphylococcal infections. It can also be used to block infection in an open skin wound, e.g. for blocking protein receptors or by immunisation. In the latter, the host produces specific antibodies which block the adherence of the bacterial strains to damaged tissue. This treatment can be used for septic arthritis and tissue damage of e.g. skin, connective tissue, and mucous membranes. Dosage for immunisation is 0.5-5 microg CBP/kg; for topical admin. the protein is used at a concn. of 25-250 microg/ml.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen binding protein; cna gene; sepsis; infection;
microbial surface component regonising adhesive matrix molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW31552 standard;
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                        (UABR-) UAB RES FOUND.
(TEXA) UNIV TEXAS A & M SYSTEM
                                                                                                          16-MAY-1996;
                                                                                                                                                            14-MAY-1997;
                                                                                                                                                                                                                20-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                   Protein
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13..159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (CBP) epitope M17, i.e. amino acids 151-297 of full-length CBP, plus a vector-derived N-terminal peptide. Claimed 441, 849 c and 1500 bp nucleic acid sequences (see AAT93436-88) respectively encode CBP epitopes M17, M31 and M55 (see AAT931552-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in screening, diagnostic and therapeutic applications including active and passive immunisation and methods for the prevention of epitopes are also contemplated for use in the preparation of vaccines and as carrier proteins in vaccine formulations, as well as in the formulation of compositions for the prevention of S. aureus infection.
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Best Local
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                                                                                                                                                           Collagen binding Ace protein; antibacterial; immunostimulant; vaccine; extracellular matrix-binding protein; lamin binding; bacterial infecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
              10-MAY-1999;
                                          10-MAY-2000; 2000WO-US12590.
                                                                                                     WO200068242-A1
                                                                                                                                                                                                          Collagen binding
                                                                                                                                                                                                                                                                                                 AAB37667 standard; protein; 458
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                                                                                                                                  Enterococcus faecalis
                                                                                                                                                                                                                                         28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                       16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein comprises Staphylococcus
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            99US-0133334
                                                                                                                                                                                                          Ace protein
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96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 830; DB 19;
Pred. No. 2.7e-62;
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Matches
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                                                                                                                                                                                                Collagen binding Ace protein; extracellular matrix-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein is an extracellular matrix-binding protein, which can bind with collagens such as collagen type 1 and type IV and with lamins. Ace protein can be used to inhibit attachment of enterococci to collagen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protective vaccines, for diagnosi infections and for screening for binding by enterococci -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New collagen-binding protein from Enterococcus, useful e.g. in protective vaccines, for diagnosis and treatment of Enterococcal infections and for screening for compounds that inhibit collagen
                                                                                  10-MAY-2000;
                                                                                                                                          WO200068242-A1
                                                                                                                                                                      Enterococcus faecalis
                                                                                                                                                                                                                                         Collagen binding Ace protein collagen binding domain.
                                                                                                                                                                                                                                                                       28-FEB-2001
                                                                                                                                                                                                                                                                                                    AAB37668;
                                                                                                                                                                                                                                                                                                                            AAB37668 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is collagen binding Ace protein from Enterococcus faecalis, where Ace is adhesion of collagen from enterococcal bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26;
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             (TEXA ) UNIV TEXAS A & M SYSTEM.
                                                       10-MAY-1999;
                                                                                                              16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
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DB; AAC83828.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pages 119-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kriekemeyer B,
1dy SR, Qin X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owens RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weinstock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHOOL.
                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178; DB 21,
Pred. No. 5.9e-07;
3; Mismatches 88
                                                                                                                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hook M, Murray BE;
                                                                                                                                                                                                cerial; immunostimulant;
lamin binding; bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΚV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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RESULT
AAW31555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to collagen binding Ace protein from Enterococcus faecalis, where Ace is adhesion of collagen from enterococcal bacteria (see AAC83828 and AAB37667). Ace protein is an extracellular matrix-binding protein, which can bind with collagens such as collagen type 1 and type IV and with lamins. Ace protein can be used to inhibit attachment of enterococci to collagen and to treat or prevent enterococcal infections, specifically as a vaccine. The present sequence is the collagen binding domain of Ace protein.
                                                                                                                                                                                     microbial surface MSCRAMM; adhesin;
                                                                                                W09743314-A2
                                                                                                                                       Key
                                                                                                                                                          Staphylcoccus
                                                                                                                                                                                                          Fibronectin;
                                                                                                                                                                                                                           Firbonectin-binding MSCRAMM derivative pCF33
                                                                                                                                                                                                                                                 21-MAY-1998
                                                                                                                                                                                                                                                                    AAW31555;
                                                                                                                                                                                                                                                                                      AAW31555 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New collagen-binding protein from Enterococcus, useful e.g. in protective vaccines, for diagnosis and treatment of Enterococcal infections and for screening for compounds that inhibit collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rich
         (UABR-) UAB RES FOUND.
(TEXA) UNIV TEXAS A & M SYSTEM
                                      16-MAY-1996;
                                                          14-MAY-1997;
                                                                             20-NOV-1997.
                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nallapareddy
                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                 159 FVNNSQAWYQEHGKEEVNGKSFNHTVHNI 187
                                                                                                                                                                                                                                                                                                                                                                                               101 YYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKIT--NEQQKE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                            64 ky---islaefeqqgygkidfv--tdndfnlrfyrdkarftsfivrytstiteagqhqat 118
                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                     FYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSN 100
                                                                                                                                                                                                                                                                                                                                       fensydinyqlnnqdatnekntsq-vknv 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-687639/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kriekemeyer B,
ddy SR, Qin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterococci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                    pCF33; collagen binding protein; sepsis; infection; rface component regonising adhesive matrix molecule; esin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                          aureus.
                                      96US-0017678.
                                                          97WO-US08210
                                                                                                                           Location/Qualifiers
1..12
                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 165.5; DB 2
30.2%; Pred. No. 1.4e-06;
                                                                                                                  "vector pQE30-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owens RT, Hool
Weinstock GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                      345
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hook M, Murray BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singh KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 146;
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ID AAW6
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                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                             Key
Peptide
05-MAR-1998
                                                                           Synthetic
                  WO9808540-A1
                                                                                    Clostridium
                                                                                                        botulism;
                                                                                                                                                         07-DEC-1998
                                                                                                                                                                            AAW68400;
                                                                                                                                                                                               AAW68400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                Antitoxin;
                                                                                                                                                                                                                                               167 kfynls 172
                                                                                                                                                                                                                                                                  158 EFVNNS
                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                49
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                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA;
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(MSCRAMM) derivative pCF33, plus a vector-derived N-terminal peptide. The invention relates to claimed nucleic acid sequences (see AAF93436-38) encoding S. aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see AAW31552-54) that confer protection against S. aureus infection. CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The epitopes are also contemplated for use in the preparation of vaccines and as carrier proteins in vaccine formulations, as well as in the formulation of compositions for the prevention of S. aureus infection. pCF33 and pDD (see AAW31556) were used to raise antends of the proteins and an aureus infection.
                                                                                                                                                                                                                                                                                                                                      Clostridium botulinum type G toxin C fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-008801/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against bovine mastitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 91; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hook M, House-Pompeo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-MSCRAMM polyclonal antibodies used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 yvntk----ddvkatltmp-ayidpenvkktgnvtlatgigstta---nktvlvdyekyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 YYSGQSAITDFEKA---FPGSKITYDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 mrgshhhhhhgsmvaadapaagtditnqltnvtvgidsgttvyphqagyvklny---gfs 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRGSHHHHHHGS----DDKVATITSGNKSTNV-----TVHKSEAGTSSVFYYKTGDM 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vpnsavkgdtfkitvpkelnlngvtstakvppimagdqvlangvidsdg---nviytftd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPEDTTHVRWF-----LNINNEKSYVS-KDITIKDQIQGGQQLDLSTLNINVTGTHSN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein comprises Staphylococcus aureus fibronectin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface component regonising adhesive matrix molecule
                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                   botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                    neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 125.5; D
30.1%; Pred. No. 0.01;
                                                                                                                                                                serotype G strain 113/30
"N-terminal His tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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                                                                                                                                                                                                                                                                    toxin
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                                                                                                                                                                                                                                                                    G; intoxication; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the histidine-tagged C fragment of Clostridium botulinum (113/30 strain) type G neurotoxin, encoded by a DNA sequence (see AAV30596) in planta perfilsb. This vector can be used to express BotG soluble C fragment in Escherichia coli host cells, with the recombinant C fragment being purified on an affinity column. The invention relates to recombinant proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat human; and other animals at risk of intoxication with clostridial toxin
Enterococcus faecalis;
detection; attenuation;
                                                 Enterococcus faecalis antigenic polypeptide fragment EF124.
                                                                                       20-APR-1999
                                                                                                                                                     AAY00241 standard; Protein; 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Preferred hosts for production of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an affinity column. derived from C. bot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-230234/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins are E. coli, insect cells and yeast cells. The recombinant toxins are used as immunogens for the production of vaccines and antitoxins that are useful in the treatment of humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV30596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and animals at risk of intoxication with clostridial toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1996;
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                                                                                                                                                                                                                                                                            VKGELKVLKQDK 208
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                                                                                                                                                                                                                                                                                                                                                                              tahqskfvv-----ydsmfdnfsinfwvrtpkynnndiqtylqneytiiscikndsgw 145
                                                                                                                                                                                                                                                                                                                                                                                                                TVDNTKNTIDVTIPQGYGS-YNSFSINY-----KTKITNEQQKEF-----VNNSQAW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                              yisnissnailslsyrggrlidssgygatmnvgsdvifndigngqfklnnse----nsni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSYVSKDITIKDQIQGGQQLDLS----TLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 120
                                                                                                                                                                                                                                                                                                                                                -YQEHGKE-----EVNGKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hhhhhhhssghi----egrhmasma---------dtiliqvf---nn 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 376-378; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams
                 faecalis;
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%;
infection; vaccine; immune response; diagnosis;
; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116; DB 13,
Pred. No. 0.098;
""ematches 75;
                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                            ----FNHTVHNI---NANAGIEGT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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AC AAYC
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AC AAYC
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DT 20-A
DT 20-B
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Ente
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                    AAY00238;
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                                                                        20-APR-1999
                                                                                                                                AAY00238 standard; Protein; 2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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06-MAY-1997;
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                                                                                                                                                                                                        337
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                                                                                                                                                                                                                                                                                                                                                  71 KDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKN-TI 129
                                                                                                                                                                                                                                                                                                                                                                                                         12 SDDKVATITSGNKSTNVTVHKS-EAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVS 70
                                                                                                                                                              10
                                                                                                                                                                                                     ddngdvvvdidhsgghatgtkgkiqlkktamd 368
                                                                                                                                                                                                                                                                                         DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG 177
                                                                                                                                                                                                                                                                                                                      ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl
                                                                                                                                                                                                                                   KSFNHTVHNINANAGIEGTVKGELKVLKQDKD
                                                                                                                                                                                                                                                                                                                                                                               sydntasytnqgssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl 228
                                                                                                                                                                                                                                                              evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
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54; Conservative
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                                                                      (first entry)
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97US-0046655.
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Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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detection; attenuation; antigenic.

Enterococcus faecalis; infection; vaccine;

immune response; diagnosis;

Enterococcus faecalis protein EF123

CA;

vaccines ç

develop

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RESULT 1
AAY00240
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AC AAY(
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DT 20-4
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide
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                                                                                                                                                                                                                                                             1014
  detection;
                                            Enterococcus
                                                                                                   AAY00240
                                                                                                                              AAY00240 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 224-225; 301pp; English.
                Enterococcus faecalis; infection; vaccine;
                                                                                                                                                                                                 1073 ddngdvvvdidhsgghatgtkgkiqlkktamd
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                                                                                                                                                                                                                             KSFNHTVHNINANAGIEGTVKGELKVLKQDKD
                                                                                                                                                                                                                                                        evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                     DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG
                                                                                                                                                                                                                                                                                                                 ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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  attenuation; antigenic.
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                                         faecalis protein EF124.
                                                                      (first entry)
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97US-0044031.
97US-0046655.
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             immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
              diagnosis;
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RESULT 12
AAY00242
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AC AAY002
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Matches 54
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
Enterococcus faecalis; infection; vaccine; detection; attenuation; antigenic.
                                           Enterococcus
                                                                                                                             AAY00242 standard; Protein; 2032 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       sydntasytnggssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl 964
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                                         faecalis
                                                                      (first entry)
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97US-0044031.
97US-0046655.
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                                         protein EF125
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DВ

Length 2032;

93; 20;

Indels

29;

Gaps

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1013

1072

immune response;

diagnosis;

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Matches 5
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06-MAY-1997;
16-MAY-1997;
Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; globulin; total serum protein; blood; hypofibrinogenaemia; cirr
                                            E.coli optimised KGF-2 mutant protein sequence.
                                                                                                                                                                                                    1073 ddngdvvvdidhsgghatgtkgkiqlkktamd 1104
                                                                                                                                                                                                                                                               1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening
                                                                           03-NOV-1999
                                                                                                                                 AAY32917 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 232; 301pp; English.
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                                                                                                                                                                                                                                                         evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 114.5;
Pred. No. 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P,
                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   .91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccines
    cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  develop
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                 albumin;
                                                                                                                                                                                                                                                                                        177
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1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 60

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:: -- Query Match Best Local S Matches 45

Local Similarity

10.1%;

Score 113.5; Pred. No. 0.0

.045;

Conservative

35;

Mismatches

3 20; ; 65;

Length Indels

47;

Gaps

9

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disease, nephrotic syndrome, trauma and crush injuries, gastrointestinal and lymphatic fistulae, and protein-losing gastroenteropathies. The methods can also be used to treat hypoglobulinaemia, total protein loss, damage to the sinus epithelium, and can be used to increase proliferation of epithelial cells of the bladder or prostate, stimulate proliferation of the salivary gland cells and to increase Goblet cell proliferation for
                                                                                                                                                                                                   vasculitis, ulcerative bowel disease, serositis, subacute bacterial endocarditis, liver disease, amyloidosis, malnutrition, malignancy, congestive heart failure, constrictive pericarditis, cardiac valvular
                                                                                                                                                                                                                                                                                                                                        gland cells, lacrimal gland cells, sinus epithelium, and Goblet cells. The methods can also be used to treat hypofibrinogenaemia caused by a cirrhosis, and disseminated intravascular coagulation (DIC). The methods can be used to treat thrombocytopaenia and to alleviate hypoalbuminaemia. These diseases are caused by: drug induced hypersensitivity, thrombocytopaenia purpura, posttransfusion purpura, metastatic tumours in the bone, aplastic anaemia, myelofibrosis, leukaemia, haemolytic syndromes, cancer chemotherapy, Zieve's syndrome, sepsis, HELLP precelamptic syndrome, megaloblastic anaemia peritonitis, congenital precelamptic syndrome, megaloblastic anaemia peritonitis, congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis; hypoalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia; leukaemia; haemolytic syndrome; Zieve's syndrome; rheumatic disease; HELLP preeclamptic syndrome; congenital rubella syndrome; systemic lupus; Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy; infection; tissue necrosis; vasculitis; ulcerative bowel disease; serositis; subacute bacterial endocarditis; liver disease; amyloidosis; congestive heart failure; constrictive pericarditis; nephrotic syndrome; congestive heart failure; constrictive pericarditis; nephrotic syndrome;
Sequence
                                                                                                                                                                                                                                                                        rubella syndrome, Epstein-Barr infectious mononucleosis, systemic lupus, preeclampsia, thyrotoxicosis, uraemia, rheumatic diseases, granulomatous processes, bacterial viral and parasitic infections, tissue necrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 5; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of keratinocyte growth factor-2 to increase levels of platelets,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jimenez P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Escherichia c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in the methods of the invention, for increasing the level platelets, fibrinogen, albumin, globulin, and total serum proto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1998;
13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             congestive heart failure; constrictive pericarditis; nephrotic sycardiac valvular disease; hypoglobulinaemia; keratoconjuctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       platelets, fibrinogen, albumin, globulin, and total serum protein in the blood. KGF-2 can also be used to stimulate proliferation of salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 keratinocyte growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrinogen, albumin, globulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a deletion mutant of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-527359/44.
                                          or preventing
  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli
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  Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0114387
98US-0074585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor-2 (KGF-2). KGF-2 fragments and mutants are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendrick
                                          keratoconjuctivitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            total serum
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                                             sicca.
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                                                                                                                                                                                                                                                                                                    granulomatous
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is sicca;
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RESULT 14
AAB10309
ID AAB103
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XW Proc
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28-FEB-1997;
13-AUG-1997;
(I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective, dermatological, gastrointestinal, hepatic, respiratory, renal and cerebroprotective activity. (I) is useful for stimulating epithelial cell proliferation in patients suffering from wound, mucositis, ulcer such as venous statis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful for treating inflammatory bowel disease, liver disorder, lung damage, diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cytoprotective; dermatological; gastrointestinal; hepatic; respiratory; renal; cerebroprotective; mucositis; treatment; epithelial cell proliferation; inflammatory bowel disease; lung damage; liver disorder; diabetes; oral injury; gastrointestinal injury; gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft; skin disorder; renal failure; brain injury; intestinal fibrosis; proctitis, female reproductive tract disorder; pulmonary fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10309
                                                                                                                                                                                                    This invention describes a novel human keratinocyte growth factor, KGF-2
                                                                                                                                                                                                                                                            Example 7; Fig 15; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA71215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1997;
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23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumonitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human KGF-2 construct pQE60-Cys37
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                                                                                                                                                                                                                                                                                                                     keratinocyte growth factor useful for promoting and accelerating healing, comprising at least 10 contiguous amino acids from a fic amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;
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Gentz
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97US-0862432.
97US-0910875.
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97US-0039045.
97US-0055561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retraction; hemopoietic syndrome; myelotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J,
Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jimenez P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coleman
, Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gruber JR;
Rampy MA;
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AC AAB6

AX PQE6

XX PQE6

XX W Iung

KW Iung

KW Puln

KW Puln

KW 11-J

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Best Local Similarity
                                                      14-JUL-1999;
15-JUL-1999;
12-AUG-1999;
19-AUG-1999;
03-NOV-1999;
22-DEC-1999;
19-APR-2000;
19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound; mucositis; ulcer; inflammatory bowel disease; liver disorder; lung damage; diabetes; oral injury; gastrointestinal injury; epidermolysis bullosa; renal failure; brain injury; proctitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61673 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                          02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2000; 2000WO-US18328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200102433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary fibrosis;
liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pQE60-Cys37 construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGKE---EVNGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kgklygskefnndcklkerie---engyntyasfn-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lfsftkyflk--iekngkvsgtkkencpysileitsveigvvavkainsnyy---lamnk 112
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                      99US-0148628.
99US-0149935.
99US-0163375.
99US-0171677.
2000US-0198322.
2000US-0205417.
2000US-9911224.
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                                                                                                                                                                                                                                                                          99US-0143648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemopoietic syndrome; ovary injury; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 113.5; DB 23.4%; Pred. No. 0.045;
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(HUMA-) HUMAN GENOME SCI INC

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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human keratinocyte growth factor (KGF-2; see AAF31901 and AAB61657). The present sequence is a KGF-2 construct protein, which was generated in the present invention. KGF-2 can be used to stimulate epithelial cell proliferation in a patient, where the patient has a wound, mucositis, an ulcer, inflammatory bowel disease, liver disorder lung damage, diabetes, oral injury, gastrointestinal injury, gut toxicity, epidermolysis bullosa, skin graft, skin disorder, renal failure, brain injury, breast tissue injury, urothelial damage, female reproductive tract disorder, intestinal fibrosis, proctitis, pulmonary fibrosis, peunrumonitis, plural retraction, haemopoletic syndrome, and myelotoxicity. In addition, KGF-2 can be used in the treatment or prevention of ovary injury, infertility, or fibrosis of the liver. KGF-2 also promotes internal healing, donor site healing, internal surgical wound healing or healing of incisional wounds made during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A polynucleotide encoding the human keratinocyte growth factor useful for stimulating epithelial cell proliferation in a patients that has e.g a wound \dot{\,}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Fig 15; 591pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF31913.
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                                                                                                                                                                                                148 ngrqmyvalngk 159
                                                                                                                                                                                                                                                                                 170 HGKE---EVNGK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                           111 FEKAFPGSKITVD-NTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NINNEKSYVSKDITIKDQIQGGQQ-------LDLSTLNINYTGT---HSNYYSGQSAITD 110 : | :: | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | mrgshhhhhhgscqalgqdmvspeatnssssfsspssagrhvrsynhlqgd---vrwrk 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AA;
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Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; score 113.5; DB 22; Length 184; 23.4%; Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                                                  -----wqh 147
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2.
2: /cgn2_6/ptodata/2.
3: /cgn2_6/ptodata/2.
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-447-031A-2
US-08-856-253-7
US-08-856-253-7
US-08-856-253-7
US-08-728-470-9
US-08-728-470-10
US-08-728-470-10
US-08-728-470-10
US-08-617-641-10
US-08-617-697-10
US-08-856-253-8
US-08-302-832-2
US-08-469-880-2
US-08-469-880-2
US-08-728-470-2
US-08-728-470-2
US-08-728-17-697-2
US-08-711-114-3
US-08-711-114-3
US-08-711-114-3
US-08-737-716-14
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            Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 18, Appli
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 Sequence
                                                         US-01
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Query Match
Best Local Similarity
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Result No.

## Sequence 4, Application US/08856253 Patent No. 6288214 GENERAL INFORMATION: APPLICANT: Hook, Magnus APPLICANT: Patti, Joseph M. APPLICANT: House-Pompeo, Karen APPLICANT: Sthanam, Narayana APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8

ALIGNMENTS

Minimum Maximum

Searched:

Sequence:

00-000-200-4
SIMANUEUNESS: TOPOLOGY: linear
TYPE: amino acid
211
н
INFORMATION FOR SEQ ID NO: 4:
TELEFAX: (512) 474-7577
TELEPHONE: (512) 418-3000
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: TAMK:193
REGISTRATION NUMBER: 33,928
ba
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: US 60/017,678
PRIOR APPLICATION DATA:
CLASSIFICATION: 514
FILING DATE: Concurrently Herewith
APPLICATION NUMBER: US/08/856,253
CURRENT APPLICATION DATA:
SOFTWARE: PatentIn Release #1.0, Version #1.30
SYSTEM:
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
ZIP: 77210
COUNTRY: U.S.
STATE: Texas
CITY: Houston
ADDRESSEE: Arnold, White & Durkee

100.0%;

Score 1122; DB 4; Pred. No. 2.1e-94;

Length

211;

	Qy 1 мксмнннннс
1;	Query Match 94.0%; Score 1054.5; DB 4; Length 512; Best Local Similarity 64.7%; Pred. No. 9.6e-88; Matches 211; Conservative 0; Mismatches 0; Indels 115; Gaps
	TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear S-08-856-253-6
	: TELEPHONE: (512) 418-5000 : INFORMATION FOR SEQ ID NO: 6: : SEQUENCE CHARACTERISTICS: : SEQUENCE CHARACTERISTICS: : LENGTH: 512 amino acids
	APPLICATION NUMBER: 1 FILING DATE: 16-MAY- ATTORNEY/AGENT INFORMAT NAME: Kitchell, Barbb
	; APPLICATION NUMBER: US/U8/856,253 ; FILING DATE: Concurrently Herewith ; CLASSIFICATION: 514 ; PRIOR APPLICATION DATA:
	OPERATING SYSTEM: PC-DC SOFTWARE: PatentIn ReleCURRENT APPLICATION DATA:
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	STATE: COUNTRY
	,
	TITLE OF INV NUMBER OF SE
	APPLICANT: Sthanam, Narayana APPLICANT: Symersky, Jindrich mitte og inventon. Offiagen einning begrein
	APPLICANT: APPLICANT: APPLICANT:
	RESULT 2 US-08-856-253-6 US-08-856-253-6 ; Sequence 6, Application US/08856253 ; Patent No. 6288214 ; Patent No. 6288214
	Db 181 NHTVHNINANAGIEGTVKGELKVLKQDKDTK 211
	QY 181 NHTVHNINANAGIEGTVKGELKVLKQDKDTK 211
	Qy 121 TYDNTKNTIDYTIPOGYGSYNSFSINYKTKITNEQQKEFYNNSQAWYQEHGKBEVNGKSF 180 
	Qy 61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 120 
	QY 1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 60
0;	Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps

Db I MRGSHHHHHGSARDISTINVTDLTVSPE  Qy 12SDKYATITSGNKSTNVTVKSE  Db 61 PTSGTVKIEGYSKTVPLTVKGEQVGAVI  Qy 12SDKYATITSGNKSTNVTVHKSE  Db 121 LTGTNTSDKYATITSGNKSTNVTVHKSE  Db 121 LTGTNTSDKYATITSGNKSTNVTVHKSE  Db 121 LTGTNTSDKYATITSGNKSTNVTVHKSE  QY 66 KSYVSKDITIKDQLOGGQOLDLSTLNIN  Qy 126 KNTIDVTIPQGYGSYNSFSINYKTKITNI  Db 181 KSYVSKDITIKDQLOGGQOLDLSTLNIN  Qy 186 NINANAGIEGTVKGELKVLKQDKDTK 21  QY 186 NINANAGIEGTVKGELKVLKQDKDTK 21  Db 241 KNTIDVTIPQGYGSYNSFSINYKTKITNI  Db 241 KNTIDVTIPQGYGSYNSFSINYKTKITNI  QY 186 NINANAGIEGTVKGELKVLKQDKDTK 21  Db 26 NINANAGIEGTVKGELKVLKQDKDTK 21  DS -08 -447 -031A - 2  US-08 -447 -031A - 2  US-0	1 MRGSHHHHHHGSAND)  12
EXHEDGKTTVKMTFDI  ITPDGAT ITFNDKVEKI  PAGTSSVFYYKTGDMLI  AGTTSNYYSGGSAITI  ITTHNYYSGGSAITI  ITTHNYYSGAWYQBI  ITHILIHILIHI  PAGTHSNYYSGAWYQBI  ITHILIHILIHI  PAGTHSNYYSGAWYQBI  ITHILIHI  PAGTHSNYYSGAWYQBI  ITHILIHIHI  PAGTHSNYYSGAWYQBI  P	DKNGKIQNGDMIKV  CSDVSGFAEFEVQG PEDTTHVRWFLNIN PEDTTHVRWFLNIN

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; MOLECULE TYPE: protein US-08-447-031A-2
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TOPOLOGY:
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Best Local Similarity
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                                                                                                                                                       APPLICATION NUMBER: US/08/856,253
APPLICATION UMBER: US/08/856,253
APPLICATION: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGERENCE/DOCKET NUMBER: TAMK:193
TETETERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                          TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
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APPLICANT: Patti, Josep
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MEDIUM TYPE: Floppy disk
                                                                                       SEQUENCE CHARACTERISTICS:
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CITY: H
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                                    STRANDEDNESS
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                                                                    LENGTH:
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                                                   amino acid
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                  linear
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Best Local S
Matches 56
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Best Local S
Matches 159
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                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 47-5577
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60,
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8
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                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/856,253 FILING DATE: Concurrently Herewit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U. ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Houston
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                                                                                                                                        TOPOLOGY:
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                                               l Similarity
56; Conser
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59; Conservative
                                                                                                                                                                       amino acid
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                                               Conservative
                                                                                                                                          linear
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                                                            11.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White & Durkee
                                                                                                                                                                                                                                                                                                                                                             US 60/017,678
                                                                                                                                                                                                                                                                                              33,928
                                               20;
                                                                                                                                                                                                                                                                                  TAMK: 193
                                           Score 125.5; DB Pred. No. 0.0009; 0; Mismatches 7
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Pred. No. 4.2e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                          DB 4;
                                               73;
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                                             Indels
                                                                              Length 345;
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RESULT 6
US-09-023-082A-30
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Sequence 30, Approx
Sequence 30, Sequence
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                                                                                                                                        FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08.
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08.
FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                    FILING DATE: 13-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 YVNTK----DDVKATLTMP-AYIDPENVKKTGNVTLATGIGSTTA---NKTVLVDYEKYG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 YYSGQSAITDFEKA---FPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
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MENDRICK, DONNA
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DUAN, D. ROXANNE
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                                MBER: US 60/055,561
13-AUG-1997
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Patent No. 592865:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
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LENGTH: 184 amino acid
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REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202_371-2600
                                                                                                                                                              APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
                       FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry
                                                                                                 FILING DATE: 16-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 NGROMYVALNGK 159
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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STREET: Bldg. J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NINNEKSYVSKDITIKDQIQGGQQ------LDLSTLNINVTGT---HSNYYSGQSAITD 110
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                                                                                  APPLICATION NUMBER:
                                                                                                                          APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                              CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
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Berkstresser, Jerry W
RATION NUMBER: 22,651
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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23.4%; Pred. No. 0.0
                                                                                  GB 9205704.1
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REFERENCE/DOCKET NUMBER:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                          FILING DATE: 530 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
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                                     FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2001 Jef
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                852 DNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 910
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                                                                                                                                                                                     APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 INNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEKAFPGSKI 120
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NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSDKVNITNQITIKAGVEGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKA----EI
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    Shoemaker and Mattare, Ltd.
    2001 Jefferson Davis Hwy., 1203 Crystal Plaza

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25.5%; Pred. No. 0.14;
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LENGTH: 1338 aming
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Best Local Similarity
                                APPLICATION NUMBER: US 08/302,832
PRIOR APPLICATION DATA:
APPLICATION DATA:
US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BEIKSTRESER', JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 01-AP
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STRANDEDNESS: sin
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                  TELEPHONE:
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    Shoemaker and Mattare, Ltd.
    Jefferson Davis Hwy., 1203 Crystal Plaza

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  (703)
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                (703) 415-0810
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25.5%;
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                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                      US/08/617,697
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5928651
GENERAL INFORMATION:
                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PORTION FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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LENGTH: 1599 amino acids
SEQUENCE CHARACTERISTICS:
                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                    FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 SDDKVATITSGNKST-----NVTVHKSEA-----GTSSVFYYKTGDMLPEDTTHVRWFLN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                              NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                      APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                      TELEPHONE:
                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001 Jefferson Davis Hwy., 1203 Crystal Plaza Bldg. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barenkamp,
                                      (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker and Mattare, Ltd
                                                      (703)
                                    415-0813
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25.5%;
                                                      415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Molecular Weight Surface Proteins of No. 5928651-Typeable Haemophilus
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                                                                                                                                                                                                                                                   US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                                         US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stephen J
                                                                                                        22,651
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                                                                                            1038-633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110.5; DI Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
     TELEFAX: (703) 415-08: INFORMATION FOR SEQ ID NO:
                                    NAME: Berkstresser, Jerry W
REGISTATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                   FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 NDNSTGLTISAKDYTVNNNYTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 1101
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Bldg. 1
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEKAFPGSK 119
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                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barenkamp, Stephen J
VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 6218141-Typeable Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker and Mattare, Ltd.
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415-0813
NO: 10:
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22.9%; Pred. No. 0.
                                                                                                                                                                                                                                                                                       US 08/302,832
                                                                                                                                                                         GB 9205704.1
                                                                                                                                                                                                                                   US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                  US/08/719,641
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                                                                                 1038-625 ·
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SEQUENCE CHARACTERISTICS:

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US-08-617-697-10
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                                                                                                                              TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2IP: 44444
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                  NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 NDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 110:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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STRANDEDNESS: si
                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2001
STREET: Bldg.
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                                                                                                                                                                     TELEPHONE:
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                                                                                   ENGTH:
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                 1600 amino acids
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                    linear
                                                                                                                                                                     (703) 415-0810
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US-08-856-253-8
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Best Local Similarity
                                                                                                             TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TA
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                         FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999 TISSDKVNITNQITIKAGVEGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKA----E 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951 ITTNASGTQKTIINGNITNEKGDLNIKNIKADAEIQIGGNISQKEGN------L 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEKAFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 VATITSGNKST----NVTVHKSEAGTSSV------FYYKTGDMLPEDTTHVRWFL 60
                                   STRANDEDNESS:
                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: Concu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
                                                                                                                                                 TELEPHONE: (512) 418-3000
                                                                                                                                                                                                       REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IT---AKNGSDLTIGNASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAG 1111
                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas
Y: U.S.
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                                                                           139 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Arnold, Wh
P.O. Box 4433
                                                                                                                               (512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Symersky, Jindrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sthanam, Narayana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              House-Pompeo, Karen
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                   linear
                                                                                                                                                                                                                                                                                                                                             Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLAGEN BINDING PROTEIN COMPOSITIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 104.5; D
22.9%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                       US 60/017,678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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Query Match Best Local Similarity

9.2%; 25.7%;

Score 103.5; DB 4; Pred. No. 0.025;

Length 139;

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                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                       943
                                   997 TISSDKINITKQITIKAGYDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAK 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TVDNTKNTIDV---TIPOGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
                                                                  61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEK----AF 115
                                                                                                                                     13 DDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDM------LPEDTTHVRWFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 KYEHGGNIIDIDFDSVPHIHG-----FNKHTEIIEED----TNKDKPSYQFGGHNSVD 119
                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                           ENGTH:
PGSKITVDNTKNTIDVTIPQGYGSYNSFSINYK ----TKITNEQQKEFVNNSQAWYQEHG 171
                                                                                                      NSKNLSITTNSSSTYRTI-----ISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRGSHHHHHHGSE---GGQNSGNQS-----
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5, 5549897
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                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BERKSTRESSER, JERRY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bldg.
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/ENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BARENKAMP, STEPHEN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker and Mattare, Ltd
Shoemaker and Mattare, Ltd
On Tefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                                                                                                                         Score 100; I
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                                                                                                                                                                       Pred. No. 1.5;
3; Mismatches
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                                                                                                                                                                                       DB 1; Length 1536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1.25
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                                                                                                                                                                         Indels 46;
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Best Local :
                                                                                                                                                                                                                                      Matches
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                             1057
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1099 KVETSG-SNNNTEDSSDNNAGL 1119
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 KEEVNGKSFNHTVHNINANAGI
 172
                                                                                                                                                                  943 NSKNLSITTNSSSTYRTI-----ISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGNL 996
                                                                                                  997 TISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAK 1056
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                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berkstresser, Jerry REGISTRATION NUMBER: 22,69 REFERENCE/DOCKET NUMBER:
                                                                                                                              61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEK----AF 115
                                                                                                                                                                                                   13 DDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDM------LPEDTTHVRWFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 16-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                   Local
                                 DGSDLTIGNT-NSADGT-----NAKKVTFNQVKDSKISADGHKVTL----
                                                   PGSKITVDNTKNTIDVTIPQGYGSYNSFSINYK----TKITNEQQKEFVNNSQAMYQEHG 171
KEEVNGKSFNHTVHNINANAGI 193
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                                                                                                                                                                                                                                   Similarity 25.:
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08302832
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Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                        1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barenkamp, Stephen J
WENTION: High Molecular Weight Surface Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker and Mattare, Ltd.
01 Jefferson Davis Hwy., 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1994
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                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                   8.9%; Score 100; DB 25.2%; Pred. No. 1.5;
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                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                      Length 1536;
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                                   -HS 1098
                                                                                                                                                                                                                                      Gaps
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Db 1099 KVETSG-SNNNTEDSSDNNAGL 1119

Search completed: January 30, 2002, 00:02:24 Job time: 2907 sec

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Result
No.
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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length: 2000000000
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ELT1_CAREL
LAC2_THACU
CYAG_DICDI
AMY_BACME
UBPB_YEAST
Y077_METUA
RPN3_YEAST
PC11_YEAST
PC11_YEAST
PC11_YEAST
PCB_CAU
DPO3_MYCPU
DPO7_BACSU
SUBF_BACSU
SUBF_BACSU
Y123_MYCPU
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ID HSER_CAVPO

AC P70106;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL DE GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) (GUANYLYL CYCLASE C).

GN GUCYZC OR GUCZC.

OS Cavia porcellus (Guinea pig).

CHARTYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 SDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSK 71
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                             PEPTIDE GUANYLIN.
CATALYTIC ACTIVITY: GT
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
         SIMILARITY:
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PS00343; GRAM_POS_ANCHORING; FAL:
Repeat; Transmembrane; Cell_wall;
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N: TYPE I MEMBRANE PROTEIN.
TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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       PROTEIN KINASE-LIKE DOMAIN
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B1.
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B3.
B3.
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Pred. No. 1.1e-69;
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S x 187 AA APPROXIMATE TANDEM REPEATS. x 187 AF APPROXIMATE TANDEM REPEATS. CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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MEMBRANE ANCHOR (POTENTIAL).
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all; 3D-structure
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InterPro; IPR001719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 2.
SMART; SM00044; CYCC; 1.
         ATL_STAAU STANDARD; PRT; 1256 AA.
P52081;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIFUNCTIONAL AUTOLYSIN PRECURSOR [INCLUDES: N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28); MANNOSYL-GLYCOPROTEIN ENDO-BETA-N-ACETYLGLUCOSAMIDASE (EC 3.2.1.96)].
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Pred. No. 2;
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GUANYLATE CYCLASE.
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REPEAT
SEQUENCE
                                                                                                                                                                                DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                                                                                                                                                                          Pfam; PF01510; Amidase_
Pfam; PF01832; Amidase_
SMART; SM00047; LYZ2; 1
                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                          EMBL; D17366; BAA04185.1; -. EMBL; L41499; AAA99982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshida T., Sugai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RN450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Staphylococcus
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95116542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium
                          790
                                                                                     Local
 60
                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs European Bioinformatics Institute. There are no restrictions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: IN THE N-TERMINAL SECTION; ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLIGOSACCHARIDE IS RELEASED INTACT.
CATALYTIC ACTIVITY: HYDROLYSES THE LINK BETWEEN N-ACETYLMURAMOYL
RESIDUES AND L-AMINO ACID RESIDUES IN CERTAIN BACTERIAL CELL-WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -[(MAN)5(GLCNAC)2]-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ENDOHYDROLYSIS OF THE DI-N-ACETYLCHITOBIOSYL UNIT IN HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR LYTIC ENZYMES
                                                                                                                                                                                                                                              wall;
                                                 KVATITSGNKSTNVTVHKSEAGTSSVF----YYKTGD-----MLPEDTTH---VRWF
 ----LNINN--EKSYVSKDITIKDQIQGGQQLDLSTLN-INVTGTHSNYYSGQSAITDFE 112
                          KIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVTKERAHGNETYVLLNNTSHNIPLGWF
                                                                             61;
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNDERGOES
                                                                                                                                                                                                                                                                                                IPR002901; Amidase_4.
                                                                                                                                                                                                                                                                                                          IPR002502; Amidase_2.
                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                       30
199
776
425
596
770
                                                                             Conservative
                                                                                                                                           AΑ;
                                                                                                                                                                   1256
775
1256
589
758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=7816834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEOLYTIC
                                                                                       8.7%;
                                                                                                                                            137384
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                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF
                                                                            39;
                                                                                                                                            MW;
                                                                           Score 98; DB
Pred. No. 9.5;
B9; Mismatches
                                                                                                                                                                              BIFUNCTIONAL AUTOLYSIN.

- ACETYLMURAMOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
1.
                                                                                                                                                                                                                                           Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROCESSING TO GENERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                           2BB76CAA292FDD20 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205-214 AND 776-792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hong Y.-M.,
                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group;
                                                                                                    1; Length 1256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELONGS
                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an N-acetylmuramoyl-L-
                                                                                                                                                                                                                                                                                                                                                                                       Usage
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RESULT
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15-DEC-1998
15-DEC-1998
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlayage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       burgdorferi.";
Nature 390:580-586(1997).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOP1_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1023 GMTLNQVAQIQAGLQYKPQVQRVPGKWTDAKFNDVKHAMDTK 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNTWISTING ENZYME) (SWIVELASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                     DNA, FOLLOWED BY PASSAGE AND REJOINING.
SUBUNIT: MONOMER (BY SIMILARITY).
MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, II
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOS
AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
                                                                                                                                                                                                                                                                                                           FAMILY.
                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHNINANAGIEGTVKGELKV------LKQDKDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDTAKYSLKAFNEQPFAVVKEQVINGQTWY--YGKLS-NGKLAWIKSTDLAKELIKYNQT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFSINYKTKITNEQQ----KEFVNNSQAWYQEHGKEEVNGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVSVGKDVYLYGTINNRTGWVNAKDLTAPTAVKPTTSAAKDYNYTYVIKNGNGYYYVTPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAFPGSKI----TVDNTK---NTIDVTIP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / B31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OMEGA-PROTEIN) (RELAXING ENZYME)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayton R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.K., Gwinn M.,
D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SFNHT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson
                                                                                                                                                                                                                                                                                                                                                    PHOSPHORUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В.,
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PRINTS; PRO0417; TOPIN; 1.

PRINTS; PRO0417; PROPISMASEI.

SMART; SM00437; TOPIAC; 1.

SMART; SM00436; TOPIBC; 1.

SMART; SM00493; TOPRIM: EMBL; TIGR; InterPro; IPR000380; Pro\_topoisomrse.
InterPro; IPR002936; Toprim.
Pfam; PF01131; Topoisom\_bac; 1.
Pfam; PF01751; Toprim; 1. use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See l or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute. InterPro; AE001180; AAC67161.1; BB0828; -. IPR003601; DNAtopI\_ATP\_bind.
IPR003602; DNAtopI\_DNA\_bind. (See http://www.isb-sib.ch/announce/ as its content Usage ρ restrictions and EMBL 18 a collaboration for outstation in commercial ö 9 its

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850

NVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGTKNQVILTGNN----IAQGTFNATK

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RESOLUTION OF SECULAR REPORT O
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Best Local
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MSN2_YEAST
P33748;
01-FEB-1994
01-FEB-1994
01-OCT-1996
                                                                                                                                                                                   "The Saccharomyces cerevisiae zinc finger pare required for transcriptional induction response element (STRE).";
EMBO J. 15:2227-2235(1996)
                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE-96208509; PubMed-8641288;
Martinez-Pastor M.T., Marchler G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-GET-1996 (Rel. 34, Last annotation update)
ZINC FINGER PROTEIN MSN2 (MULTICOPY SUPPRESSOR M$N2 OR YMR037C OR YM9532 02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.

Isomerase; Topoisomerase; DNA-binding; Complete proteome.

RCT_SITE 324 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 848 AA; 97663 MW; 37DEA5FBLE12FA2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Odell C., Bowman S., Submitted (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estruch F., Carlson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93309420; PubMed=8321194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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                      FUNCTION: POSITIVE TRANSCRIPTIONAL FACTOR THAT ACTS AS A COMPONENT OF THE STRESS RESPONSIVE SYSTEM. RECOGNIZES AND BINDS TO THE STRESS RESPONSE ELEMENT (STRE) WHICH IS INVOLVED IN THE RESPONSE TO VARIOUS FORMS OF STRESS (HEAT, OXIDATIVE, OSMOTIC, ETC.). INVOLVED IN THE REGULATION OF THE CTT1, DDR2, HSP12 GENES. SUBCELLULAR LOCATION: NUCLEAR.
     SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous zinc finger genes identified by multicopy suppression SNF1 protein kinase mutant of Saccharomyces cerevisiae."; Cell. Biol. 13:3872-3881(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKGLKDTVMQLEPKIDSSEFRTVIESQKI---ENKNSINYTINIGKYGPYLIFKGHNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOSAITD------FEKAFPGSKITVDNTKNTIDVTIPQG-YGSY-----NSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFKLNNTLMPTIKGAAVINLLEKYFPVLIELNFTSNMEEKLDKIAIGKLDKIKYLSKFYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSK-DITIKDQIQGGQQLDL----STLNINVTGTH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INAKTPLENLYKKDEIEKIINEKELKPNILGVDPLTGLNVIFKNTIYGNIVQLGEDTHAP
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  EGR
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Pred. No. 7
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PROTEINS
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databases
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R EMBL; Z48502; CAA88403.1; -.

R PIR; A48131; A48131.

R PIR; S39004; S39004

R PIR; S39004; S39004

R HSSP; P08047; 1SP1.

R TRANSFAC; T01257; -.

R InterPro; IPR00022; Znf-C2H2.

R InterPro; IPR00022; Znf-C2H2.

R PARNYS; PR00046; ZINCFINCER.

R PRINYS; PR00046; ZINCFINCER.

R SMARY; SM00355; Znf-C2H2; 2.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.

R DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Act
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Best Local
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                                                                                      P3904b;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-2095 (Rel. 40, Last annotation update)
MURAMIDASE-2 PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-MURAMIDASE-2 PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-MURAMIDASE-2 PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-MURAMIDASE-2 PRECURSOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics in the European Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
                                                           Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.,
                                                                            Enterococcus hirae
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                                                                                                                                                                                                                                                                            ELKVLKQDKDTK 211
:| | ||:| |
DL-VNKQDEDPK 472
                                                                                                                                                                                                                                                                                                                                                                                                                         DFEKAFPGSKITVDNTKN---TIDVTIPQGYGSYN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDTNSYSNSISNSNSNSTGNLN----SSYFNSLNIDSMLDDYVSSDLLLNDDDDDTNLSR 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSK
                                                                                                                                                                                                                                                                                                                                           NAMTKINPSQQLQQQLNRVQHKQLTSSHNNSSTNMKSFNSDLYSRRQRASLPIIDDSLSY
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647
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279
665
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AND
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                                                            Bacillus/Clostridium
SEQUENCE OF
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ASP-RICH (
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; I
Pred. No. 6.
                                                                                                                                                                                                      PRT;
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50-73
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                                                           group;
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                                                            Enterococcaceae,
                                                                                                         (PG-HYDROLASE-2)
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Query Match
Best Local S
Matches 49
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J. Gen. Microbiol. 139:3099-3117(1993).
-I- FUNCTION: MAY WORK IN CONCERT WITH AND POTENTIATE THE PROCESSIVE HYDROLYTIC ACTION OF MURAMIDASE-1, WHICH REQUIRES BINDING OF THE ENZYME TO NONREDUCING ENDS OF GLYCAN CHAINS. HYDROLYSIS IN THE ENZYME TO NONREDUCING ENDS OF GLYCAN CHAINS. HYDROLYSIS IN THE NUMBER OF BINDING SITES
                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                     SMART; SM00257; Lysm; 6.
SMART; SM00047; LYZ2; 1.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002901; Amidase_4.
InterPro; IPR002482; Lysm.
Pfam; PF01832; Amidase_4; 1.
Pfam; PF014/6; Lysm; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Del Mar Lleo M., Canepari P., Satta G.;
Thermosensitive cell growth mutants of Enterococcus hirae that
"Thermosensitive cell growth mutants are stimulated to divide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The second peptidoglycan hydrolase covalently binds penicillin.";
J. Bacteriol. 171:4355-4361(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
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MEDLINE=89327152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequence analysis of the muramidase-2 gene
Enterococcus hirae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M77639; AAA24776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 9790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolinger D.L., Daneo-Moore L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 9790;
MEDLINE=92165737;
                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR MURAMIDASE-1. MAY FUNCTION IN FACILITATING SEPTUM FORMATION AND CELL SEPARATION. ACTIVE ON M.LUTEUS CELL WALLS AND ON E.HIRAE CELL WALL FRACTIONS, BUT NOT ACTIVE ON E.HIRAE INTACT CELL WALLS. CAN COVALENTLY BIND PENICULLIN.

CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN N-ACETYL-D-GLUCOSAMINE AND N-ACETYLMURAMIC ACID IN PEPTIDOGLYCAN HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.

SUBCELLULAR LOCATION: SECRETED.

DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES SIMILARITY: CONTAINS 6 LYSM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A42296; A42296.
; P21697; 1PCS.
    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
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50
257
338
414
489
    Conservative
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K
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                                                                                                                                           531
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607
                     8.5%;
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LYSM 2.
LYSM 3.
LYSM 4.
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LYSM 5.
LYSM 5.
LYSM 5.
LYSM 6.
LYSM 6.
LYSM 6.
                     Score 95;
Pred. No.
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Mismatches
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC REGION.
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STRAIN=KIZ / MG1655;

STRAIN=KIZ / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland P., Biley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                   Moszer I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus
"Escherichia coli K-12.";
Biochimie 73:1361-1374(1991).
-i- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL the Fundament Bioinformatic Institute There are no restrict the Turner and the EMBL the Swiss Institute There are no restrict the Turner Bioinformatic Institute There are no restrict the Turner Bioinformatic Bioinfo
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Best Local
                                                                                   Campbell K., Collins M.D., East A.K.;

(Rucleotide sequence of the gene coding for Clostridium botulinum (Clostridium argentinense) type G neurotoxin: genealogical comparison with other clostridial neurotoxins.";

Biochim. Biophys. Acta 1216:487-491(1993).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
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EMBL; AE000237; AAC74487.1; ALT_SEQ.

EMBL; D90778; BAA1509.1; ALT_SEQ.

EMBL; D90778; BAA18880.1; ALT_SEQ.

EMBL; D90779; BAA18881.1; ALT_SEQ.

EMBL; X62680; -; NOT_ANNOTATED_CDS.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
BOTULINUM NEUROTOXIN TYPE G PRECURSOR (EC 3.4.24.69) (BONT/G)
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MEDLINE=94092745; PubMed=8268233;
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Clostridium botulinum.
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            ENDOPEPTIDASE.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L)
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL AC
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHAN
FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTIRDSVFTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSADGATKWQYNH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDGKDSTGT--EINGNNG-----KVI-QDGD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITVDNTKNTIDVTIPQGYG----SYNSFSINY--KTKITNEQQKEFVNNSQAWYQEHGKEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGELVITGDNATVNNNGKTTVDGKDSTGTEINGNNGK-VIQDGDLDVSGGGHGIDITGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQQL----DLSTLNIN------VTGTHSNYYSGQSAITDFEK-----AFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTS---SVFYY---KTGDMLPEDTTHVRWFLNI-----NNEKSY--VSKDITIKDQIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHHRNNSPLPPTPPDDESDDTPVPPTPGGDEIIPDDPDDTPTPPKPVSFNNDVILDKTEK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHHHHHG-----SDDKVATITSGNK------STNVTVHKSEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVDN-KGTMTVTDPESMGIQIDGDKAIVNNEGESTITNGGTGTQINGDDATANNNGKTT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%;
                                                                                                                                                                                                                                                                                                                           Bacillus/Clostridium group; Clostridiaceae;
SECRETED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
(BY
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                             CHANNEL
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                                                         AND
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                                                                                                                                                                                                                 P78032;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN)
UNITALISTING ENZYME) (SWIVELASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
METAL
ACT_SITE
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SEQUENCE FROM N.A
STRAIN-ATCC 29342
MEDLINE-97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X74162; CAA52275.1; -. HSSP; P04958; 1AF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                            Mycoplasmataceae;
                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                          Mycoplasma pneumoniae.
                                                                                                                                                                                                       TOPA OR MPN261 OR MP572.
                                                                                                                                                                                                                                                                                                                                                                                                         MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1004 YINKWFSITITNDRLGNANIYINGSLKKSEKILNLDR 1040
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                                                                                                  NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotoxin; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          838 DSIPFDLSLYTKDTILIQVF---NNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSD 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 DMLP-----EDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLS----TLNINVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGS-YNSFSINY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KTKITNEQQKEF-----VNNSQAW-YQEHGKE-----EVNGKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYSIKDNISD 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FNHTVHNI---NANAGIEGTVKGELKVLKQDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
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1296
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                                                   N.A.
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229
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233
449
  / M129;
PubMed=8948633;
                                                                                                                            Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%;
23.0%;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOTULINUM NEUROTOXIN G, HEAVY-CHA
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
MW; DC8E47E15F665C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.5;
Pred. No. 21;
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                                                                                                                                                   group;
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OXIN G, HEAVY-CHAIN.

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1296;
                                                                                                                                                      Mollicutes;
                                                                                                                                                                                                                                                     (RELAXING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 10
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Best Local Similarity
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Nucleic Acids Res. 24:4420-4449(1996).

**Nucleic Acids Res. 24:4420-4449(1996).

**I FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO INDEPENDENT BREAKAGE OF ANOTHER.

**CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

**I CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

**I SUBUNIT: MONOMER (BY SIMILARITY).

**I SIMULTANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

**SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-C4_Topoisom; 2.
PF1NTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1AC; 1.
SMART; SM00433; TOP1BC; 1.
SMART; SM00433; TOPRIM; 1.
  OPAH_NEIGO
Q04884;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P06612; 1ECL.
InterPro; IPR003601; DNAtopI_ATP_bind.
InterPro; IPR003602; DNAtopI_DNA_bind.
InterPro; IPR000380; Pro_topoisomrse.
InterPro; IPR002936; Toprim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
ISomerase; Topoisomerase; DNA-binding; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000056;
HSSP; P06612; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 THVRWELNINNE-----KSYV------SKDITIK-DQIQGGQQLDLSTLNI
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                                                                                                                                                                           AEGSIQRVKKEKE 618
                                                                                                                                                                                                                      VKGELKVLKODKD
                                                                                                                                                                                                                                                                       GEQVNEELSKHFGKIINKEFTKN-----MEKSLDEIAENKKNYQEFLRDFWSNFKEEVKL
                                                                                                                                                                                                                                                                                                                     TKITNEQ------QKEFVNNSQAWYQEHGKEEV--NGKSFNHTVHNINANAGIE-GT
                                                                                                                                                                                                                                                                                                                                                                     TARQTHPAARYTQASLIEALEK---
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1G 624 652

1G 673 702

1TE 340 340

1CE 711 AA; 81965 M
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(Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB96220.1;
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340 D
81965 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rmatics Institute. There are no rest institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE 1.
C4-TYPE 1.
DAA CLEAVAGE (BY SIMILARITY).
, 16B863588B06582E CRC64;
                                                                                                                                                                                                                                                                                                                                                                     -SNIGRPSTYNTMASVNLDRGYASLNKHAFHVTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                   238
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MSI1 / F3;
MEDLINE=93178439; PubMed=8440254;
MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
Kupsch E.-M., Knepper B., outer membrane proteins account for the cell control opacity (Opa) outer membrane proteins account for the cell control opacity (Opa) outer membrane proteins account for human leukocytes and
                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Stern S., Kupsch E.-M., Meyer T.F., Swanson J.; Mol. Microbiol. 6:1073-1076(1992).
-i- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE PROTEINS ARE IMPLICATED IN PATHOGENESIS AND AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The opacity proteins of Neisseria encoded by a family of 11 complete Mol. Microbiol. 5:1889-1901(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z18939; CAA79372.1; -. EMBL; X60711; CAA43121.1; -. PIR; S28631; S28631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F., Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=MS11 / V18;
MEDLINE=92114767; PubMed=1815562;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPACITY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92261323; PubMed-1584024;
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-KAFPGSKI---
                                                                         KW-----NNNKYSVNIE-NVRIRKENGIRIDRKTENQENGTFHAVSSLGLSAIYDFQINDK 130
                                                                                                                                                                                                                 SHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVF----YYKTGDMLPEDTTHVR
                                                                                                                                                                   AYAYEHITHDYPEPTAPNKNKISTVSDYFRNIRTRSVHPRVSVGYDFGGWRIAADYARYR 75
                                                                                                                   -WFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFE----
                                                                                                                                                                                                                                                                   45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003394; Opacity.
                                                                                                                                                                                                                                                                                                                                                                                  234
238
238
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238
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-TVDNTKNTIDV-TIPQG--YGSYNSFSINYKTKITNEQQKEFVN 161:::::: : | | | ::::
                                                                                                                                                                                                                                                                                  8.2%;
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Last annotation update)
PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                              Score 91.5; D
Pred. No. 3.6;
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPACITY PROTEIN OPA60.
SED -> MLKA (IN MS11 / V18).
V -> M (IN MS11 / V18).
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genes.";
                                                                                                                                                                                                                                                                                          3.6;
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                                                                                                                                                                                                                                                                                                              Length 238;
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RE SUBJECT
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                                                                        ACT_SITE
ACT_SITE
SEQUENCE
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P29019;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOGLUCANASE PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE)
                                                                                                              CHAIN
                                                                                                                                                 PROSITE; PS00812; GLYCOSYL_HYDROL_F8; 1.
Cellulose degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                               EMBL; M68872; AAA22409.1;
PIR; A44808; A44808.
HSSP; P04955; ICEM.
                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91259037; PubMed-2045781; Ozaki K., Ito S.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELLULASE) (ENDO-K).

Bacillus sp. (strain KSM-330).

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID-1409;
                                                                                                                                        SIGNAL
                                                                                                                                                                          Pfam; PF01270; Glyco_hydro_8; PRINTS; PR00735; GLHYDRLASE8.
                                                                                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Gen. Microbiol. 137:41-48(1991).
-I- FUNCTION: THIS ACID ENDOGLUCANASE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Purification and properties of an acid endo-1,4-beta-glucanase from Bacillus sp. KSM-330.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ozaki K., Sumitomo N., Ito S.; "Molecular cloning and nucleotide sequence of the gene encoding endo-1,4-beta-glucanase from Bacillus sp. KSM-330."; J. Gen. Microbiol. 137:2299-2305(1991).
                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92121880; PubMed=1770347;
                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
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                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: ONE TRP RESIDUE HAS BEEN PROVED TO BE THE MECHANISM OF ACTION OF ENDO-K.
SIMILLARITY: BELONGS TO CELLULASE FAMILY D (FAMILY 8
                                                                                                                                                                                                                                                                                                                                                                                                                  LINKAGES IN CELLULOSE.
PTM: THE N- AND THE C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ENDOHYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                   HYDROLASES).
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                                                                        56
130
191
463
             Conservative
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463
130
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51882
                       8.1%;
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           31;
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Pred.
                                                                     PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (POTENTIAL).
407FA54F5236C59E CRC64;
                                                                                                              ENDOGLUCANASE
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           Mismatches
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No.
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                                    DB 1;
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           64;
                                    Length 463;
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           Indels
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RESULT 12
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AC Q50274
AC Q50274
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DT 20-AUG
CC Mycopl
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RP SEQUEN
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20-AUG-2001
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Q50274;
                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      Bhugra B., Voelker L.L., Zou N., Yu H., Dybvig "Mechanism of antigenic variation in Mycoplasma site-specific DNA inversions.", Mol. Microbiol. 18:703-714(1995).
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STRAIN=KD735-15;
MEDLINE=20245550; PubMed=10781561;
Shen X., Gumulak J., Yu H., French C.T.,
"Gene rearrangements in the vsa locus of
J. Bacteriol. 182:2900-2908(2000).
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIPOPROTEIN A PRECURSOR.
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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MEDLINE-21267165; PubMed-11353084;
Chambaud I., Hellig R., Ferris S., Ba
Moszer I., Dybvig K., Wroblewski H.,
                          EMBL; U23947;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blanchard A.;
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SIMILARITY: BELONGS TO THE PULMONIS LIPAB LIPOPROTEIN FAMILY.
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                                                                                                                                                   "Cloning of two new cry genes from Bacillus thuringiensis wuhanensis strain.";
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                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PESTICIDIAL CRYSTAL PROTEIN CRYIGB (INSECTICIDAL
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                                              -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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                                                                                                     r. Microbiol. 40:227-232(2000).

FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PIERIS RAPAE. DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
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                 SWISS-PROT entry is copyright. It is produced through a collaboration
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N-ACYL DIGLYCERIDE (POTENTIAL).

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                          EMBL; X57834; CAA40967.1;
EMBL; Z68221; CAA92494.1;
PIR; A41267; A41267.
HSSP; P17678; 1GAU.
                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1995) to the EMBL/GenBank/DDBJ-I- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF GENREGION, INCLUDING VITELLOGENIN GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-91342668; PubMed=1875944;
Spieth J., Shim Y.H., Lea K., Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Creat 01-DEC-1992 (Rel. 24, Last 20-AUG-2001 (Rel. 40, Last TRANSCRIPTION FACTOR ELT-1.
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Pfam; PF00555; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELT-1 OR W09C2.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 VTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDL
                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTKITNEQQKEFVNNSQAWYQEHGKEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNTCESN--RGYGDYTPLPAGY
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                                                                                                                                                                                                                                                                           the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonically expressed Caenorhabditis elegans to the GATA transcription factor family."; Biol. 11:4651-4659(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ELEYFPETDKVWI-EIGETE 1154
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24.5%;
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                                                                           ALT_INIT
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Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R., Blumenthal T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416
                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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WormPep; W09C2.1; CE03799

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Best Local S
Matches 45
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PROSITE: PS00114; GATA_ZN_FINGER_2; 2.
Transcription regulation; Activator; D
Nuclear protein.
217 241 GATA_TYPE
ZN_FING 272 296 GATA_TYPE
SEQUENCE 272 296
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2_THACU STAN
LAC2_THACU STAN
Q02075;
01-WOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96171523; PubMed=8598061; Wahleithner J.A., Xu F., Brown K.M., Brown S.H., Halkier T., Kauppinen S., Pederson A., Schneider "The identification and characterization of four plant pathogenic fungus Rhizoctonia solani."; Curr. Genet. 29:395-403(1996).
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ZN_FING
SEQUENCE
                            This
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SMART; SM00401; ZnF_GATA;
PROSITE; PS00344; GATA_ZN
PROSITE; PS50114; GATA_ZN
     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitosporic Ceratobasidiaceae;
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                                                                    COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

SUBCULT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: SECRETED.

TISSUE SPECIFICITY: IN MYCELIA, AT A LOWER LEVEL THAN LCC4.

SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                        PRODUCTS (PROBABLE).

CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) =
                                                                                                                                                                                                                                                                                                                                                          FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
                            SWISS-PROT
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     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 (Rel. 35, Created)
97 (Rel. 35, Last sequence update)
97 (Rel. 35, Last sequence update)
97 (Rel. 35, Last annotation update)
PRECURSOR (EC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)
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0320; GATA; 2.
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  Swiss
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ry is copyright. It is produced through Institute of Bioinformatics and the EN
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## SUMMARIES

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MEDLINE-20407335; PubMed-10948146;
MEDLINE-20407335; PubMed-10948146;
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray I "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of
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Enterococcus
                                      Enterococcus faecalis (Streptococcus faecalis). Bacteria; Firmicutes; Bacillus/Clostridium grou
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EMBL; AF260873; AAG23932.1:
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MEDLINE-20407335; PubMed-10948146;
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray B "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules for production of ace during it.
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EMBL; AF260877; AAG229335.l; -.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor: 1
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STRAIN-MD9/TX0249;
MEDLINE-20407335; PubMed=10948146;
MEDLINE-20407335; PubMed=10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules, from different strains of enterococcus faecalis and evidence for production of ace during
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                                                                                                Gram_pos_anchor;
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                                                                         GRAM_POS_ANCHORING;
     31
78842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
68848
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28.3%;
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Bacillus/Clostridium
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Last annotation update)
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Pred. No. 1.2e-05;
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                           POTENTIAL
     1CA8A1D98CE69392 CRC64;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2040/333; Function MEDLINE-2040/333; Function R.W. Mallapareddy S.R., Singh K.V., Duh R.W. "Diversity of ace, a gene encoding a mirecognizing adhesive matrix molecules, recognizing adhesive matrix molecules for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PARKER/TX2619;
MEDLINE=20407335; PubMed=10948146;
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                                                                                            VEGEASGNONV
                                                                                                                                       IEGTVKGELKV 203
                                                                                                                                                                                                                   QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSENHTVHNINANAG 192
                                                                                                                                                                                                                                                                                                                                                                              TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS 170
                                                                                                                                                                                                                                                                                                                                                                                                                          TITSGNKSTNVTVHKSEAG---TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT
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                                                                                                                                                                                                                                                                                                                                IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                          RDKARFTSFIVRYTSTITEAGQHQATFENSYDINYQLNNQDATNEKNTSQV-----KNVF
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ilarity 28.3%;
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les, from different strains of
for production of ace during )
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No. 1.5e-05;
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Q9F856;
01-MAR-2001
01-MAR-2001
01-MAR-2001
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STRAIN-B-343/TX2783;
MEDLINE-20407335; PubMed-10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface componen "Diversity adhesive matrix molecules, from different strains o recognizing adhesive matrix molecules for production of ace during
                                                                                                                STRAIN-VARIOUS STRAINS; MEDLINE-20407335; PubMed-10948146; Meinstock G.M., Murray Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules, from different strains of the strain
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seguence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                     enterococcus faecalis and infections.";
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Bacteria; Firmicutes;
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AF260895;
AF260880;
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AF260896; AAG23954.1; -.
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                                                              68:5210-5217(2000).
AAG23953.1;
AAG23938.1;
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Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (Streptococcus faecalis).
Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 Q9XBQ7;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                    Collagen.
                                                                                                                                                                                                                          Rich R.L., Kreikemeyer B., Owens R.T., Weinstock G.W., Murray B.E., Hook M.; "Ace: a collagen-binding MSCRAMM from E J. Biol. Chem. 0:0-0(1999).

EMBL; AF159247; AAD43342.1; -.
HSSP; Q53654; IAMX.
                                                                                                                                                                                                                                                                                                 STRAIN-CG110;
                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITSGNKSTNVTVHKSEAG----TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT
                                                                      TATATORLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGEASGNQNV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEGTVKGELKV 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY 225
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                        IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY
                                              IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP
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458 AA;
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                                                                                                                     Conservative
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Bacillus/Clostridium group; Enterococcaceae;
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                                                                                                                                Score 178; DB 2; Pred. No. 1e-05;
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Pred. No. 6.5e-06;
3; Mismatches 88
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                                                                                                                                                                                                                                                                faecalis.
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COLLAGEN ADHESIN PRECURSOR.
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MEDLINE-20407335; PubMed-10948146;
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murra
"Diversity of ace, a gene encoding a microbial surface compone
"Diversity of ace, a gene encoding a microbial surface compone
recognizing adhesive matrix molecules, from different strains
recognizing adhesive matrix molecules, from different strains
                                                                       ACE.
  Bacteria; Fin
Enterococcus
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Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inrect. Immun. 68:5210-5217(2000). EMBL; AF260878; AAG23936.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LBJ-1/TX0020;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                      VEGEASGNQNV 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS
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1 (TrEMBLrel. 17,
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63948 MW;
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28.3%;
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                      (Streptococcus faecalis).
Bacillus/Clostridium grou
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7CD61EAD3FDA0993 CRC64;
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Q9F864; O1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                  Signal.
SIGNAL
                                                                                                                                                                                                                                 STRAIN-MC02152/TX0024;
MEDLINE-20407335; PubMed=10948146;
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray E
"Diversity of ace, a gene encoding a microbial surface component
recognizing adhesive matrix molecules, from different strains of
enterococcus faecalis and evidence for production of ace during l
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SIGNAL
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                                                                          InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                       EMBL; AF260876; AAG23934.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis Bacteria; Firmicutes;
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InterPro; IPR001899; Gram_pos_anchor
Pfam; PF00746; Gram_pos_anchor; 1.
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EMBL; AF260879; AAG23937.1; -.
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          SEQUENCE
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                                                                                                                                                                                  Immun. 68:5210-5217(2000).
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28.3%;
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Bacillus/Clostridium group; Enterococcaceae;
          MW;
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POTENTIAL.; C9B368AE30858359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 178; DB 2;
Pred. No. 1.3e-05;
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STRAIN-SESS/TXI329;
MEDLINE-20407335; PubMed-10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray B "Diversity of ace, a gene encoding a microbial surface component "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of recognizing matrix molecules, from different strains of recognizing matrix molecules, from different strains and recognizing matrix matrix molecules, from different strains and recognizing matrix molecules and recognizing matrix molecules and recognized matrix molecules and 
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01-MAR-2001
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Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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EMBL; AF260875; AAG23933 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLAGEN ADHESIN
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                                      IEGTVKGELKV
                                                                                  RDKARFTSFIVRYTSTITEAGQHQATFENSYDINYQLNNQDATNEKNTSQV-----KNVF
                                                                                                                           QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                                                                                                                                      IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY
                                                                                                                                                                                                               IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP
                                                                                                                                                                                                                                                            TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS
                                                                                                                                                                                                                                                                                                     TITSGNKSTNVTVHKSEAG----TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT
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Pred. No. 1
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Pred. No. 1
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AFDC039BFD47C356 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, C)
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=WH245/TX0635;
MEDLINE=20407335; PubbMed=10948146;
MAILIAPAREDDY S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray
"Diversity of ace, a gene encoding a microbial surface component
recognizing adhesive matrix molecules, from different strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9F858;
Q9F858;
01-MAR-2001
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MEDLINE-20407335; PubMed=10948146;

Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murra

"Diversity of ace, a gene encoding a microbial surface compone

recognizing adhesive matrix molecules, from different strains
enterococcus faecalis and evidence for production of ace durin
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F260891; AAG23949.1; -.
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Q9EU80; UTEMBLTel. 16,
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01-MAR-2001 (TIEMBLTEL. 16,
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MAIDLINE-20407335; PubMed=10948146;
Mailapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M.,
"Diversity of ace, a gene encoding a microbial surface or
recognizing adhesive matrix molecules, from different str
enterococcus faecalis and evidence for production of ace
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                      TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS 170
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QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                     IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY 225
                                                                                                IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                           t. Immun. 68:5210-5217(2000).
AF260892; AAG23950.1; -.
AF260884; AAG23942.1; -.
AF260885; AAG23943.1; -.
AF260886; AAG23944.1; -.
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                                                                                                                                                                                                                                                 Score 175; DB 2;
Pred. No. 1.1e-05
4; Mismatches 8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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				22 AAF58257		22 AAF58252		13 AAQ24123	19 AAT93438	19 AAT93437	DB ID		SUMMARIES
Oligonucleotide Di	Oligonucleotide Di	Oligonucleotide D2	Oligonucleotide D2	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1	Collagen binding p	p16 and cCOLR6A as	Collagen binding p	Collagen binding p	Description		

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5,4	5.4	5.4	5.4	5.4	5.4		5 5						5.6	5.7	5.7	5. 8	5. 8	5. 8	6.0	6.0	6.0	6.0	6.0	6.0	6.7	6.9		7.1	19.1	19.1	19.1	19.1	19.1
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22	17	21	21	11	21	21	21	21	20	21	21	18	21	21	21	22	21	21	20	21	20	20	20	20	21	22	22	20	22	22	22	22	22
AAH24065	AAT41852	AAA70156	AAA70105	AAQ03875	AAA70106	AAA70212	AAA70170	AAA70112	AAX99503	AAA70117	AAZ98287	AAT72882	AAA70236	AAA70096	AAA70207	AAC93000	AAA70152	AAA70211	AAX99560	AAA70107	AAX33184	AAX33180	AAX33182	AAX33181	AAC83828	AAF58238	AAF58238	AAX13327	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254
Yeast AOD9604-asso	cDNA encoding Plas	Plasmodium falcipa	Plasmodium falcipa	Sequence encoding	Plasmodium falcipa		Plasmodium falcipa	Plasmodium falcipa	Nucleic acid seque			Plasmodium var-7 g	Plasmodium falcipa		Plasmodium falcipa	Candida albicans C	Plasmodium falcipa	Plasmodium falcipa	Nucleic acid seque	Plasmodium falcipa		Cowpox virus bsr f	sequence of	Base sequence of t			Oligonucleotide D1	Enterococcus faeca		Oligonucleotide D2		Oligonucleotide Dl	Oligonucleotide D1

## ALIGNMENTS

RESULT AAT93437

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AAT93437;

AAT93437 standard; DNA; 849

ВP

CDS Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRANM; adhesin; vaccine; immunisation; diagnosis; therapy; epitope M31; ss. Hook M, WO9743314-A2 Staphylcoccus aureus. Collagen binding protein M31 epitope DNA. 21-MAY-1998 (first entry) (UABR-) UAB RES FOUND. (TEXA ) UNIV TEXAS A & M SYSTEM. 16-MAY-1996; 14-MAY-1997; 20-NOV-1997. House-Pompeo K, Patti JM, 96US-0017678 97WO-US08210 Location/Qualifiers 253..849 /\*tag= a Sthanam N, Symersky J,

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Best Local S
Matches 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that confer protection against S. aureus infection. These nucleic cacid sequences can be used in the recombinant production of the CBP cepitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in C screening, diagnostic and therapeutic applications including active and passive immunisation and methods for the prevention of bacterial colonisation in an animal such as a human. These DNA segments and the peptides encoded by them are also contemplated for use in the preparation of vaccines and as carrier proteins in c vaccine formulations, as well as in the formulation of compositions of the prevention of S. aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This nucleic acid comprises a portion of the Staphylococcus aureus cna gene that codes for collagen binding protein (CBP) epitope M31 (see AAW31553), i.e. amino acids 61-343 of full-length CBP. Claimed 441, 849 and 1500 bp nucleic acid sequences (see AAW31532-54) respectively encode CBP epitopes M17, M31 and M55 (AFB 34831552-54)
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mes 849; Conserv
                                                                                                                                                                                              CTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAAAGTTAT
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                                                    ACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATT
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 ACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACACA
                                   acattaaacattaatgtgacaggtacacatagcaattattatagtggacaaagtgcaatt
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This nucleic acid comprises a portion of the Staphylococcus aureus cna gene that codes for collagen binding protein (CBP) epitope M55 (see AAW3154), i.e. amino acids 30-531 of full-length CBP. Claimed 41, 849 and 1500 bp nucleic acid sequences (see AAT93436-38) respectively encode CBP epitopes M17, M31 and M55 (see AAM931552-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The Claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                       Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                        Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
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Best Local Similarity Matches 849; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAGTGGCATGGCCGACAAGC
                                                                                                                                                                GAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGATTTAAGC
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                       GATACCAAG 849
                                                           GCTAATGCCGGTATTGAAGGTTAAAAGGTGAATTAAAAGTTTTAAAACAGGATAAA
                                                                                                                                                                                                                                                 ACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATCAA
                                                                                                                                                                                                                                                                                                                                  ATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACAAA 660
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                                                                                                                                           gagcatggtaaggaagtgaacgggaaatcatttaatcatactgtgcacaatattaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 A; 198 C;
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Pred. No. 1.1e-176;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologous p16 and cCOLRÉA inserts) comprises a structure resembling a signal sequence. Following this region, a region called A (tag- h) is found followed by a repetitive stretch of 187 amino acids called B: (tag- i), B2 (tag- j) and B3 (tag- k). Directly following these regions there is a region called W (tag- l) which consists of a repetitive, hydrophilic structure contg. several proline residues. This region is thought to mediate the binding of the protein to the cell wall. The amino acid sequence nearest to the C-terminal end consists of a long stretch of hydrophobic residues followed by some charged amino acids (tag- n). This region is called M (tag- m).
                                                                                                                                                                                                                                                                          1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybrid DNA molecule encoding S.aureus protein is expressed in E.coli and use septic arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amino acid encoded by homologous pl6 and cCOLR6?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guss BM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG
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DB; AAR22675.
                                                                                                                                                                                                                                                                                                                                                  AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGCAA
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                                           TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATATAGTGGACAAAGT
                                                                                       atatgctaccaagaagatacgacacatgtacgatggtttttaaatattaacaatgaaaaa
                                                                                                                                                                 ATATGCTACC-AGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAA
                                                                                                                                                                                                              ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT
                                                                                                                                                                                                                                                                                                                                    aaattaagtgatgtttcgggatttgcagaatttgaagtacaaggaagaaatttaacgcaa
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 GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG
                                                                                                                                                                                                                                          A--CGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAA---CGGGAG
                                                                                                                                                                                                                                                                      acaaatactttagatgacaaagtagctacgataacatctgggaataaatcaacgaatgtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 1946 A; 675 C; 869 G; 1122 T; 0 other;
                                                                                                                                                                                                                            90SE-0003374
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97.78;
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used for diagnosis e
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This nucleic acid comprises a portion of the Staphylococcus aureus cna gene that codes for collagen binding protein (CBP) epitope M17 (see AAM31552), i.e. amino acids 151-297 of full-length CBP. Claime 441, 849 and 1500 bp nucleic acid sequences (see AAM3436-38) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1891
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                                                                                                                                                                                                                                                                                                                                                                                              Antibody that interacts with collagen binding domain Staphylococcal cna gene product - useful to prevent I in animal infected with Staphylococcus aureus
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epitope M17; ss.
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                                                                                                                                                                                                                                                                                                                                                Claim 40;
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                                                                                                                                                                                                                                                                                                                                          Page 113; 143pp; English
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Best Local
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                      26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                      01-FEB-2001
                                                                                                              WO200107665-A2
                                                                                                                                                            Electron-transfer group;
                                                                                                                                                                                                   Oligonucleotide D1835
                                                                                                                                                                                                                                                                             AAF58252 standard;
                                                             26-JUL-2000;
                                                                                                                                                                                                                            24-APR-2001
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(CLIN-) CLINICAL MICRO SENSORS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 ATAACATCTGGGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGGAACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGTTAATAATTCACAAGCT 711
                                                                                                                                                                                                                                                                                                                                                                                                       TCATATAATAGTTTTTCAATTAACTACAAAACCAAAATTACGAATGAACAGCAAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATAACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGG
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                                                                                                                                                                                                                                                                                                                                          tttgttaataattcacaagct 441
                                                                                                                                                                                                                                                                                                                                                                                            tcatataatagtttttcaattaactacaaaaccaaaattacgaatgaacagcaaaaagag
                                                                                                                                                                                                                                                                                                                                                                                                                                            aaaataactgttgataatacgaagaacacaattgatgtaacaattccacaaggctatggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCAAGGTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACAT
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                                                             2000WO-US20476
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                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                             936
                                                                                                                                                                        ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                             ВP
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Pred. No. 1.2e-87;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Umek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, us
                                                                                                                                                                                                                                                                      491
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AAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTA 778
                                                                 AAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATC
                                                                                        CAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACA
                                                                                                                                 TTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACA
                                                                                                                                                                              GCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAA
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                                                                                                                                                                                                                                                                    TGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAAAGTT
                                                                                                                                                                                                                                                                                                                  TTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAGATA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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NO. 2.1e-28;
NO. 25
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RESULT 6
AAF58254/c
ID AAF58254 standard; DNA;
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                    monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159728/16
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17-MAR-2000; 2000US-0190259.
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                                                                                                              731
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              AAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATG
                                                                              AAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGC
                                                                                                                                          AGGTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAG 178
                                                                                                                                                                                                        GCGGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAAC 118
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                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                       20.0%; Score 170; DB 22; Length 936; llarity 1.0%; Pred. No. 2.1e-28; Conservative 524; Mismatches 254; Indels
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                                                                                                                                                                                                                                                                                                                                                    expression.
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RESULT 7
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ID AAF582
XX AAF582
XX AAF582
XX AAF582
XX DI 24-APR
XX DE Oligon
XX Electr
KW gene e
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XX W02001
XX 26-JUL
PR 26-JUL
PR 26-JUL
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XX DRR WPI; 2
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                WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                    Oligonucleotide D1954.
                                                Umek RM;
                                                                                                                                                                                         01-FEB-2001
                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                   Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                           26-JUL-1999;
17-MAR-2000;
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                                                                            (CLIN-) CLINICAL MICRO SENSORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTA
                                                                                                                                                                                                                                                           CAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACA
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                                                   ATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAGGATA
                                                                                                                                                       AAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936 BP; 5 A; 142 C; 7
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Pred. No. 2
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2.1e-28;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 936 BP; 6 A; 138 C; 8 G; 8 T;
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17-MAR-2000; 2000US-0190259
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  TTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAGATA
                                                                                                        AAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATG
                                                                                                                                                                                                                   AAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGC
                                                                                                                                                                                                                                                                                                                            AGGTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAAC
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524; Mismatches
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2.1e-28;
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 Example 6;
                            Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single gurface.
                                                                     WPI; 2001-159728/16
                                                                                                                                      26-JUL-1999;
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 Page 128;
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17-MAR-2000; 2000US-0190259.
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Pred. No. 2.1e-28;
24; Mismatches 254;
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17-MAR-2000; 2000US-0190259.
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)

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                                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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gene expression; ss.
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Electron-transfer group; ETM; mismatch; genotyping;
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                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                    monitoring gene expression.
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                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses of a single surface.
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Query Match
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Conservative

19.1%; Score 162.4; DB 0.5%; Pred. No. 9.7e-27 tive 522; Mismatches 2

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. ≆	TAATGCCGGTATTGAAGGTACTGTAAAAGGTG	783	Qy
3	5 พพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพ	666	Db
č	GCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAA	723	Qy
₹	5 พพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพ	606	망
Ä	CAAAATTACGAATGAACAGCAAAAAGAGTTTC	663	Qy
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Ö	TGATGTAACAATTCCACAAGGCTATGGGTCATAATAATA	603	Qy
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· 🗃	TGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTG	543	Qy
*	WWWWWW	426	Db
G	ATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGAC	. 483	Qy
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C	ATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAG	423	Qy
€ .	5 жининининининининининининининининининин	306	Ф
• ⊢	ACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATG	363	Qy
₹	5 เพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพ	246	DЬ
н	GGTTCATAAAAGTGAAGCGGGAACAAGTAGTC	303	Qy
2	wwwwwwwwwwww	186	DЬ
C	AAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGG	243	Qy
E	5 พพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพพ	126	р
Ö	ATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAG	183	Qy
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- 5	GGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAG	123	Qy
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Search completed: January 29, 2002, 23:13:49 Job time: 3798 sec

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US-08-232-463-1

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100	ication US/0885625  114  1710N: TTION: Natti, Joseph M. House-Pompeo, Karen thanam, Narayana ymersky, Jindrich, NATION: COLLAGEN B NATION: AND METHOD UENCES: E ADDRESS: Arnold, White & D O. Box 4433  ton O. Box	6049 60049 60049 60049 1689 11689 11689 8457 8457 6150 6150 150 150 150 150 150 150 150 150 150
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RESULT 2
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                                                                Sequence 5, Application US/08856253 Patent No. 6288214 GENERAL INFORMATION:
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Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich
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Matches 849; Conserv
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CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, VGURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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STREET: P.O. B
CITY: Houston
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COUNTRY: U.
ZIP: 77210
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           FILING DATE: 22-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861/804

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707

FILING DATE: 22-OCT-1991

PRIOR APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PATTI, JOSEPH
APPLICANT: SIGNAS, Christer
APPLICANT: SWITNLSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL
TITLE OF INVENTION: ITS PREPARATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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NAME: McGowan, Malcolm REGISTRATION NUMBER: 39
                                      APPLICATION NUMBER: SE 9003374-7 FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATACCAAG
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P.O. Box 1404
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JONSSON, Hans
LINDBERG, Martin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 835-6520
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3827 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 849; Conserv
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            GCTAATGCCGGTATTGAAGGTACTGTAAAAAGTTGAAAAAGTTTTAAAACAGGATAAA
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                                                                   GAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAAT
                                                                                                                        ACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATCAA 720
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                                                    GAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAAT
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; LOCATION:
US-08-447-031A-8
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US-08-447-031A-8
                                                                                                                                                                                                                                                            NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 0128

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEPHONE: (703) 836-2021

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                         Query Match 93.3%;
Best Local Similarity 97.8%;
Matches 836; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08447031A Patent No. 5851794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/447,031A
FILING DATE: 22-MAX-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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APPLICANT:
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1171 GATACCAAG 1179
MOLECULE TYPE: DNA (genomic) FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SWITALSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL
TITLE OF INVENTION: ITS PREPARATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
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HOOK, Magnus
JONSSON, Hans
LINDBERG, Martin
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SIGNAS, Christer
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                                                                         Score 792.2; DB 2; Pred. No. 2.4e-180; O; Mismatches 13;
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DR-856-253-1 Squence 1, Application US/08856253 Stent No. 6288214 SENERAL INFORMATION: APPLICANT: Hook, Magnus APPLICANT: House-Pompeo, Karen APPLICANT: Sthanam, Narayana APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee	GATAAAGATACCAAG 849               GATAAAGATACCAAG 1965	ATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAG 83 	TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAAT 77. 	TACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGG 714 	AACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC 65-	GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG 59 	TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT 53. 	AGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGAT 474	ATATGCTACC-AGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAA 414 	ACGGTTCATAAAAGTGAAGCGGAACAAGTAGTGTTTTCTATTATAAACGGGAG 35 	ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 30	AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGCAA 240 	GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180 	GGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG 12:
		<b>4</b> 50	<b>4</b> 90	30	70	10	50	<b>4</b> 90	30	70	10	0 50	90	30

STREET: P.O. Box 4433

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RESULT 6
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US-08-856-253-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: TAN
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 6:
-FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STALL:
COUNTRY: U.L.
77210
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Best Local Similarity
Vatches 27; Conserve
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: DC COMPOS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE_DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                            1294
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                                                                                                                                                                                                                                                                                            161 CATTCAATGATAAAGTAGAAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTAC 220
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ZIP: 22313-0299
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TELEFAX: (703)683-4109
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TTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTG 460
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                                                                      ATTATAAAACGGGAGATATGCTACCAGAAGATACGACACGTGTACGATGGTTTTTAAATA 400
                                    VA
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1800 Diagonal Road, Suite
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26-AUG-1991
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Sequence 13, App. ...
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Best Local Similarity
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APPLICANT: Sim, K
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                          15404 АТАТСТАТТТАТАТТААААААСБААТАТАААААСБААТТТАТТАБАААТСБААБАБАБДАД 15463
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
ANTI-SENSE:
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TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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530 AAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATA 589
                                                                                                                                                                                     354 AGATATGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTTAACAATGAAAA 413
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REFERENCE/DOCKET NUMBER: NIH121.001CP1
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                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19124 base pairs
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                               AAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGA 473
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Miller, Louis H.
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Chitnis, Chetan
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16th
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RESULT 8
5231168-1
; Patent No. 5231168
; Patent No. 5231168
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PAI
TITLE OF INVENTION MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATE
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Best Local Similarity 42.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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TTATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAAT 575
                                                          aatagtagaggttgaagaaattctaccagaagataaaaatgaaaaagttcaacatgaaat 1784
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US-08-960-780-51
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; Patent No. 62044
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                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                        REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U5/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PATOR APPLICATION DATA:
PATOR SAMPLES
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                 STRANDEDNESS:
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2421 N.W. 41st Street, Suite A-1
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Narva, Kenneth E.
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Best Local Similarity
Matches 128; Conserv
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                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT:
ATTORNEY/AGENT INFORMATION:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                       CLASSIFICATION:
                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                             COUNTRY:
                  FILING DATE:
                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   STATE:
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2421 N.W. 41st Street, Suite A-1
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Finstad-Lee, Stacey
VENTION: No. 6242669el Pesticidal Toxins and Nucleotide
VENTION: Sequences Which Encode These Toxins
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Narva, Kenneth E.
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                  MBER: US 08/960,780
30-OCT-1997
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47.4%;
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                                                                                                                                                                                          Version #1.30
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Bacillus laterosporus
US-09-371-913A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-371-913A-2
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                     APPLICANT: Stury 1.5,
APPLICANT: Stury 1.5,
TITLE OF INVENTION: Pesticida.
TITLE OF INVENTION: Strains
TITLE OF INVENTION: "TURER: U!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09371913A Patent No. 6297369
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/371,913A CURRENT FILING DATE: 1999-08-10 PRIOR APPLICATION NUMBER: 60/095,955 PRIOR EILING DATE: 1998-08-10 PRIOR APPLICATION NUMBER: 60/138,251 PRIOR EILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 AATAACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 CAATTATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAA 572
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACGATTAATTCTGATGCAATGGCACAGTTTAAAGAACAATTTTTAGATAGGGATATTAA 527
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Stockhoff, Brian A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Walz, Mikki
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  5.0%;
47.4%;
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Score 42.8; DB 4; Pred. No. 0.091;
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                    Length 1341;
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                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 25-MAR-
                                                                                                                                                                                                                                               FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
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                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                               TELEPHONE:
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                                                                                                   NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hawthorne
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577,
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                                 919-541-8689
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Koziel, Michael G
Mullins, Martha A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desai, Nalini M
Kostichka, N. Kristy
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                                                   919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                      UMBER: US 08/037,057
25-MAR-1993
                                                                                                                                                                                                               23-MAR-1994
                                                                                                                                                                                                                                                                                     US 08/314,594
                                                                                                                                                                                                                                US 08/218,018
                                                                                                                                                                                                                                                                                                                                                             US/08/471,033
                22:
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                                                                                      CGC 1695/CIP3/DIV7
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PRIOR APPLICATION DATA:

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NAME/KEY: CDS
LOCATION: 1..4038
OTHER INFORMATION:
CTHER INFORMATION:
US-08-471-033-22
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US-08-471-044-22
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Patent No. 5840868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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                                                           APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                  STREET:
CITY: H
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Local Similarity 47.4%;
hes 128; Conservative
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                 ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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Kostichka, N. Kristy
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Koziel, Michael G
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product"
                                                                                               US/08/471,044
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                                                                                                                                     Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142;
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                                                                                                                                                                                                                          Sequence 22, Patent No. 5
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Best Local Similarity
                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                              APPLICANT:
                                                                                                                                                   APPLICANT:
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4041 base pair
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                                                          APPLICANT:
                                                                             APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: linear
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REGISTRATION NUMBER: 40,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
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                                                                                                                                                                                                                              5849870
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                                                        Desai, Nalini M
Kostichka, N. Kristy
Duck, Nicholas B
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                                                                                                                                               Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
                                                                                                              Carr, Brian
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                                                                                                                             Nye, Gordon J
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product"
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Pred. No. 0.12;
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Best Local Similarity 47.4%;
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/
FILING DATE: 09-SEP-194
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 23-MAR-194
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEPAX: 919-541-8689
FORMATION FOR CEC.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,483A
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PRIOR APPLICATION DATA:
US 08/314,594
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LENGTH: 4041 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
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                                                                                                                 633 ATATAATAGTTTTTCAATTAACTACAAAAC 662
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                                                                          549 GTTTGATAGTTATCTAGATACGCATTTAAC 578
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LOCATION: 1..4
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                                                                                                                                                                                                                                                      CAATTATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTTCCAGGTTCTAA 572
                                                                                                                                                                                                                                CACCTATAAAAATGTGGAACCGACAACAATTGGATTTAATAAATCTTTAACAGAAGGTAA
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product"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,046A
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4041 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
TITLE OF INVENTION: Protein Genes
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0: FILING DATE: 25-MAR-1993
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APPLICATION NUMBER: US 08/463,483
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                  393 TTTAAATATTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGAT 452
309 TATAAAGACAAATTATAAAGAAATTACTTTTTCTATGGCAGGCTCATTTGAAGATGAAAT 368
                                                                                                                                                                       LOCATION: 1..4038
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: CG
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Kostichka, N. Kristy
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Koziel, Michael
                                                                   Conservative
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